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SEARCH REQUEST FORM

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Requester's Full Name: RITA	IN MITRA	Examiner #: 77995 Date: 7/8/02
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If more than one search is subr		**************************************
Please provide a detailed statement of the	search topic, and describe	
known. Please attach a copy of the cover		
Inventors (please provide full names):	encoding	the same"
- Jugory Donoho C	Alexander Ti	urner, Michael Nohla Glenn Frie-
Earliest Priority Filing Date:	19/1999	when Michael Nchles Glenn Frie-
For Sequence Searches Only Please inclu appropriate serial number.	, de all pertinent information ((parent, child, divisional, or issued patent numbers) along with the
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Page

2222222222 goitre, hypoglycaemia, diabetes mellitus, endometriosis, pulmonary embolism and muscular dystrophy. Antibodies to disorders such as these can be made by providing a polypeptide of the invention to an immuno-competent vertebrate and harvesting blood or serum from the anaphylaxis, hepatitis, multiple sclerosis, cancer, coronary artery disease, malaria, atopic dermatitis, amyotrophic lateral sclerosis, meningitis, attention deficit disorder, Crohn's disease, gastroanteritis,

G 905 ..

cDNA; 3594 BP Matches 1688; Best Local Sequence 3594 BP; Local Similarity Conservative 958 A; 810 C; 921

Human: "ANGO 229: T cell; heart; liver; pancreas; placenta; brain; lung; skeletal muscle; kidney; spleen; lymph node; peripheral blood leukocyte; bone marrow; thymus tissue; abnormal blood coagulation; asthma; cancer; anaphylaxis; hepatitis; multiple sclerosis; coronary artery disease; ss; malaria; atopic dermatitis; amyotrophic lateral sclerosis; meningitis; attention deficit discreder; Crohn's disease; gastroenteritis; optire; hypoglycaemia; diabetes mellitus; endometriosis; pulmonary embolism; 07-SEP-2001 (first entry)

Homo sapiens muscular dystrophy; immuno-competence; vertebrate; blood; serum.

mat_peptide sig_peptide /*tag- b 174..2216 /product= 72..173 Location/Qualifiers 72..2219 reag-"Human TANGO

19-OCT-1999; (MILL-) MILLENNIUM PHARM INC 23-JUN-2000; WO200129088-A1 2000WO-US17386 99US-0420707 /product-"Mature human TANGO 229

New isolated nucleic acid molecule for diagnosis, therapy of human and other animal disorder, or as regulating Mackay CR, 2001-308477/32. DB; AAU00670. cellular Myers PS, Kirst Fraser 3 Leiby KR; prevention, modulating agent for and

processes

This protein and similar others exhibit the ability to affect growth, proliferation, survival, differentiation, activity, morphology, or movement/majoration of, e.g. T cells and cells of the heart, liver, pancreas, placenta, brain, lung, skeletal muscle, kidney, spleen, lymph node, peripheral blood leukocyte, bone marrow or thymus tissue. They can be used as modulating agents for regulating cellular processes, thus the proteins and their associated nucleic acids can be used to proposition the provent, diagnose, or treat disorders associated with physiological The sequence represents a cDNA which encodes human TANGO 229 polypeptide Claim 1; Fig 1; 263pp; English

disorders include abnormal blood coagulation

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                                                                                                                                                                                                                                                                                 Matches 1620;
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                                                                                                                                                                                                                                                                                                                                                                                        disease. The polynuc polities may also be used in screening for drugs effective in the treatment of symptomatic or phenotypic manifestations of perturbing the normal function of NHP in the body. Nucleotide constructs encoding NHP products are used to genetically engineer host cells to express such products are used to genetically engineer host cells to express such products in vivo. These host cells allow for the identification of compounds that bind to NHP receptors or trigger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence represents a polynucleotide which encodes a novel human protein (NHB) contraining a CUB domain (an extracellular domain). CUB proteins have been associated with regulating development, modulating cellular processes and preventing infectious disease. NHB nucleotide sequences are useful for gene therapy of physiological disorders or diseases. NHB pulliponucleotides are useful as hybridisation probes for screening libraries and assessing gene patterns. NHB nucleotide sequences are useful for detecting mutant or inappropriately expressed NHBs (for example, those proteins associated with obesity which blood pressure, connective tissue disorders and infertility) for the disposis of a financial connective tissue disorders and infertility for the disposis of a financial connective tissue disorders and infertility.
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                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                     422 G;
                                                                                                                                                                                                                   {cactggcgcgggctgccgggcggggcctcctg
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                                                                                                   caatgacatctaagaattatcccggg
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                                                                                                                                                                                                                                                                             Indels
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               441
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Claim

8; Fig 1; 263pp; English

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481
                                                                                  421
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                                                                                                                                                                                    408
                                                                                                                                                                                                                     301
                                                                                                                                                                                                                                       348 SGDESNNHKPREWLEIDLGEKKKITGIRTTGSTQSNFNFYVKSFVMNFKNNNSKWKTYKG
                                                                                                                                                                                                                                                                                      241
rkkkkgspygsaeaqktdcwkqikypfarhqsaeftisydnekemtqkldlitsdmag
                      RKKKKKGSPYGSAEAOKTDNWKQTKYDFARHOSAEFTISYDNEKEMTOKLDLITSDWAG
                                                                                                                                                       IVNNEEKVENGNSNERDEVONNEIPPIVARYVRVPOTWHORIALKVELIGCOITGGNDS
                                                                                                             LVWRKTSQSTSVST
                                                                                                                                              ivnneekviggd
                                                                                                                                                                                                     sydssnipkprewieidlyekkkitgirttystysninfyvksivmniknnnskwktykg
                                                                                                                                                                                                                                                                                      GSLSDKRPLFTSNGCSRSLSFEPDGQIRASSSWQSVNESGDQVHWSPGQARLQDQGPSWA
                                                                    \{ {f lsdkrflftsngcsrslsfepdgqirassswqsvnesgdqvhwspgqarlqdqgpswa} \}
                                                                                                                                   infrdpvqnnfippivaryvrvvpqtwhqrialkveligcqitqgnds
                                                                                                      KEDETITRPIPSEETSTGINITTVAIPLVLLVVLVFAGMGIFAAF 527
                                     586
                                                                       480
                                                                                                                                       420
                                                                                                                                                                      467
                                                                                                                                                                                                        360
                                                                                                                                                                                                                                       407
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The sequence represents human TANGO 229 polypeptide. This protein and care in the shilling to affect growth, proliferation, convival, differentiation, activity, morphology, or movement/migration of, e.g. Teelis and cells of the heart, liver, panceas, placenta blood leukocyte, bone marrow or thymus tissue. They can be used a portion of the dispose, or treat disorders associated with physiological processes. Cand their associated nucleic acids can be used to promosticate, prevent, conditions, or treat disorders associated with physiological processes. These disorders include abnormal blood coagulation, sathma, anaphylaxis, can be partitis, multiple sclerosis, cancer, coronary artery disease, malaria, cateful disorder, croim's disease, gastroenteritis, goitte, hypoglycaemia, diabetes melitius, endometriosis, pulmonary embolism and comproviding a polypeptide of the invention to an immuno-competent correction of the providing a polypeptide of the invention to an immuno-competent coverbrate and harvesting blood or serum from the vertebrate.

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AAU00670
                    AAU00670;
                                  AAU00670 standard; Protein; 715
                                                     w
(first entry)
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밁 Ş 밁 Ş 밁 9 맑 Qy В γ

07-SEP-2001

Human, TANGO 229; T cell; heart; liver; pancreas; placenta; brain; lung; skeletal muscle; kidney; spleen; lymph node; peripheral blood leukocyte; bone marrow; thymus tissue; abnormal blood coasquiattion; asthma; cancer; anaphylaxis; hepatitis; multiple scierosis; coronary artery disease; malaria; atopic dermatitis; amyotrophic lateral sclerosis; meningitis; attention deficit disorder; Crohn's disease; gastroenteriis; molire; hypoglycaemia; diaboties mellitus; endometriosis; pulmonary embolism; Human TANGO 229 polypeptide

NAME OF TAXABLE AND CONTRACT O

dystrophy; immuno-competence; vertebrate; blood;

serum

Location/Qualifiers

48 MVPGARGGGALARAAGRGLLALLLAVSAPLRLQAEELGDGCGHLVTYQDSGTMTSKNYPG $\verb|mvpgargggalaraagrgllalllavsaplrlgaeelgdgcghlvtygdsgtmtsknypg|$ 107

Gaps

Matches 538; Query Match

Local

Similarity

92.1%; Score 2812; DB 22; 100.0%; Pred. No. 2.8e-243;

Length

Conservative

0,

Mismatches

Sequence

715

0

407 360

SGDSSNNHKPREWLEIDLGEKKKITGIRTTGSTQSNFNFYVKSFVMNFKNNNSKWKTYKG

 $\tt gslsdkrflftsngcsrslsfepdgqirassswqsvnesgdqvhwspgqarlqdqgpswa$

347 300

240

180

287

120

288 GSLSDKRFLFTSNGCSRSLSFEPDGQIRASSSWQSVNESGDQVHWSPGQARLQDQGPSWA

228 VAGDISGNAVDGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRYEGILANGVLSRD

vagdisgnmvdgyrdtsllckaaihagiladelggqisvlqrkgisryegilangvlsrd

181

121 168 108

TYPNHTVCEKTITVPKGKRLILRLGDLDIESQTCASDYLLFTSSSDQYGPYCGSMTVPKE 167

typnhtvcektitvpkgkrlilrlgdldiesqtcasdyllftsssdqygpycgsmtvpke

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61

IVNNEEKVFQGNSNFRDFVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGCQITQGNDS sgdssnnhkprewieidlgekkkitgirttgstqsnfnfyvksfvmnfknnnskwktykg

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361 408 301 348 241

밁 Š 밁 õ 밁 S 밁 6 밁 Ş В

467

LVWRKTSQSTSVSTKKEDETITRPIPSEETSTGINITTVAIPLVLLVVLVFAGMGIFAAF 527

528 RKKKKKGSPYGSAEAQKTDCWKQIKYPFARHOSAEFTISYDNEKEMTQKLDLITSDWA 585

481 538

В, ğ 밁 Ş

> 421 468

AUU00628 standard;

Protein;

487

B

S S S S E S

00628;

New isolated nucleic acid molecule for diagnosis, therapy of human and other animal disorder, or as regulating cellular processes

prevention, and modulating agent

Mackay CR,

Myers PS,

Kirst

, LS

Fraser 3

Leiby

2001-308477/32. DB; AAS00660.

(MILL-) MILLENNIUM PHARM INC

19-OCT-1999;

23-JUN-2000; 2000WO-US17386

WO200129088-A1

Domain Protein Domain Peptide HOMO Sapiens

/note-/note=

"Cytoplasmic domain" "Transmembrane domain' "Mature human TANGO 229"

. 480

/note- " 35..715 /note= 35..45

"Extracellular domain" "Signal peptide"

. 455

29-AUG-2001 (first entry)



Ş,

139 gW

1384 accadggtaargattcattggtgtggcgcaa--gacaagtcaaagcaccagt 1434

9tcccccagacatggcaccagaggatagccttgaaggtggagctcattggttgccagatt 1383 ccncagacatggcaccaaaggatagccttgaaggaggagctcattggatgccagatt 198

p

Page

10

199 -cacaagg aatgattcattgngagtggtgcancganaagtcagagcaccagt 250

AAZ32182 standard;

cDNA;

6893

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RESULT
AAH367
                                                                                                                                                  Ouery Match
Best Local Similarity
                                                                                                                                     Matches 189;
                                                                              1206 gaagacctataaaggaattgtgaataa-tgaagaaaagdtgtttcagggtaactctaact 1264
                                                                                                                                                                                                                                                                                                expression. For example, N and W may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally. N may be used to produce the colon cancer:associated Ps, by inserting the nucleic acids into a host cell and oulturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and Analy 1789 represent sequences used in the exemplification of the recent caracteristics.
                                                                                                                                                                                                                                   N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.\
                                                                                                                                                                                                                  Sequence 252 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diagnass associated with inappropriate P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH32943 to AAH37195 and AA\$73514 to AAG77788 represent human colon cancer associated nucleic add molecules (N) and proteins (P), when
          1265 ttogggacccagtgcaaaacaatttcatccctcccatcgtggccagatatgt-gcgggtt 1323
                                                                                                                                                                                                                                                                                              present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the proteins are collectivel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-SEP-1999;
03-NOV-1999;
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                                                                            19
                                                                 gnggacctatanaggaattgtgagtaagagaataaaaggtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-235357/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          colon cancer antigen
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gacccacatycacnycaynncatacctcccatnytyychayatatytcycyyatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lon cancer; colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preventing,
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                                                                                                                                   Conservative
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990S-0163280
                                                                                                                                                                                                              68 A; 56 C; 68 G; 47
                                                                                                                                                7.2%;
81.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g 4277 human
diagnos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 human colon cancer-associated polypeptides,
agnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         803pp; English.
                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoding cDNA SEQ ID NO:3818.
                                                                                                                                              Score 127.2; DB ;
Pred. No. 6.9e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       known as colon cancer antigens. The colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      molecules (N) and proteins (P),
                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen CA
                                                                                                                                                                                                              13 other;
                                                                                                                                                             DB 22;
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                                                               tntcaggggaactctaact
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                                                                                                                                     Matches
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958

1018 caggaccaaggcccatcatgggcttcgggcgacagtagcaaccaccacaaccacgagag 107;

gcttcttcgtttaagaaatcttggtggggagattactgggaacccttccgtgcccgtctg 6385 tggcagtcggtcaatgagagtggagaccaagttcactggtctcttggccaagcccgactt 1017 6266 aatggatgttccacacccctgggtatggaaaatggaaagatagaaaacaagcaaatcaca 6325

898 aatggttgcagcagatccttgagttttgaacctgacgggcaaatcagagcttcttcctca 957

Sequence 6893 BP; 2090 A; 1700 C; 1423 G; 1680 T; 0 other

Local Similarity

5.4%;

249;

Conservative

0, Score Pred.

Mismatches

Indels

6; Gaps

ļ,

94.4; DB 20; Length 6893; No. 8.7e-14;

to some of the reference alleles.

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polymorphic stace as given in a table in the specification, selected from 92 single nucleotide polymorphisms in which the nucleotide at the polymorphic stee is different from a nucleotide at the same stee in a reference allele. The nucleic acids, and primers and probes, are used to identify polymorphisms, which may predispose an individual to disease, especially a vascular disease. They can also be used in penotype correlations, forensics, paternity testing, medicine or genetic analysis. AAY49500 to AAY49573 represent the proteins which correspond
                                                                                                                                                                                                                                              AAZ32159 to AAZ32194 represent reference alleles for specifically claimed nucleic acid sequences from the present invention which comprise
                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 26; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 Determination of polymorphisms in genes, especially those identifying predisposition to vascular disease \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-620066/53
P-PSDB; AAY49563.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; coding sequence polymorphism; vascular pathology gene; polymorphic site; phenotype correlation; forensic; paternity testing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human coagulation factor V nucleotide sequence
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                   The probes/primers given in AAR03921-31 are used to amplify and/or detect mutations in human Father-V DNA esp. in DNA encoding the APC binding and/or Yeavage s
                                                                                        Screening for genetic defect associated with thrombosis anticoagulant response to activated protein C - useful homozygosity or heterozygosity for a mutation in Factor
  Sequence 6909
                                                            Claim 16; Page 60-65; 98pp; English
                                                                                                                                    WPI; 1995-293134/38.
                                                                                                                                                                                                                                                                                                                                                                                                        3920
                                                                                                                                                                                                                                                                                                                                                                                                                                               6740
                                                                                                                                                         Bertina RM,
                                                                                                                                                                                                14-FEB-1994;
                                                                                                                                                                                                                                                           WO9521938-A1
                                                                                                                                                                                                                                                                                                                                 Human
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                                                                                                                                                                                                                   14-FEB-1995;
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                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                   activated
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                                                                                                                                                                                                                                                                                                           thrombosis; thrombophilia; diagnosis; anticoagulant;
                                                                                                                                                                                                                                                                                                 rotein-C; APC; homozygosity; heterozygosity; ss.
                                                                                                                                                       Reitsma PH
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BP; 2096 A; 1700 C; 1430 G; 1683
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Query Match Best Local Similarity

51.0%;

Score Pred.

92.8; DB 16; No. 2.3e-13;

Langth 6909,

gene therapy protocols

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New transgenic mice expressing activated protein C resisfant factor V and factor V null transpenic mice useful for screening antocopylants as models for human thrombophilia and as models for testing in utero
                                                                                                                                                                                                                                                                                                                                  Factor V; FV; activated protein C; APC activated protein C resistant factor V thrombophilia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                Human factor V cDNA sequence SEQ ID
                                                                                                                                        (UNMI ) UNIV MICHIGAN
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\thrombosis; screening;
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AAB24216 ene segr-032802

Page

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rsqnefpagtegttaspdirnttvtpnvtkdvalaavlvpvlvmvlttlililvcawhwr coagulation cofactor; haemostatic; coagulation related disorder; 533 us-09-691-344a-4.rag οy Ş 밁 õ 밁 Ş 밁 Ş 밁 Ş 밁 В 242 182 414 358 464 414 KVEQGN NERDEVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGCQ-----ITQ- 463 354 NHK 548 WKQIKYPF-298 kifqgnkdj TSNGCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSN 353 ----GNDSLVW ppprnsnd----lkd tpnvtkdvalaavlvpvlv ----VAIPLVLLVV Rtsgcygtlgmesgviadpqitassvlewtdhtgqenswkpkkarlkkpgppwaafatde 241 PREWLEIDLGEKKKITGIRTTGSTQSNFNFYVKSFVMNFKNNNSKWKTYKGIVNNEE 413 Accession NO. _şwlqidlnkekkitgiittgstmvehnyyvsayrilysddgqkwtvyrepgveqd qdvrnnflppiiarfirvnptqwqqkiamkmellgcqfipkgrppkltqp KTSQSTSVSTKKEDETITRPI------PSEET--STGINITT- 505 tappklakgrapkftqplqprssnefpaqteqttaspdirnttv VFAGMGIFAAF----RKKKKKGS---PYGSAEAQKTDC vlttlililvcawhwrnrkkktegtydlpyw----SAEFTISYDNEKEMTQKLDLITSDMA 585

RESULT AAY70539

7 nrkkkt

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534

474

-RKKKKGS---PY 537

<u>:-</u> egtydlpy 547

H

AAY70539 standard;

Protein;

669

A

04-JUL-2000 AAY70539;

(first entry)

cerebroprotective; thaemophilia; stroke;

screening.

Human; Factor 8 Homblogue; F8H; cerebroprotective; therapeutic; Human Factor 8 Homologue

Rosteck PRJ, (ELIL) LILLY & CO ELI. 2000-256580/22. DB; AAZ51872. homolog polypeptides and coagulation related disc Su W, 9805-009852 Ľ nucleic acids encoding them for general for a stroke

31-AUG-1998; 20-AUG-1999; 09-MAR-2000 WO200012532-A1 Homo sapiens.

99WO-US19047

RESULT AAB24216

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AAB24216;

AAB24216 standard; protein;

889

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06-FEB-2001

(first entry)

qs

Soluble neuropillin sNP-2 protein sequence SEQ ID NO:4.

soluble neuropillin

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470 wkgmkqflpakavdheetpvryssse--vnhlsprevttvlqadsaeya 516

dragw

469 547 413

357

297

Claim 3; Page 64-66; 68pp; English

treating Factor 8

The present sequence is a human Factor 8 homologue (FBH), a coagulation cofactor which is selectively expressed in haematopoletic, heart and reproductive tissues. It has haemostatic and cerebroprotective activities. The FBH Contains a Factor 5/8 signature and is useful as a therapeutic for treating coagulation related diseases such as hemophilia and stroke. The nucleic acid is useful as hypridisation probe and amplification primer for detecting deficiencies in the level of FBH maken, for screening FBH gene mutations and for monitoring regulation of gene expression. Pragments of the nucleic acid are also useful as diagnostic probes and hyprogrammers, and can be used in screening methods such as those using DNA chips; The present sequence is also useful as a target to screen therapeutically useful modulators

Query Match Best Local : Matches 190; 124 GKRLILRLGDLDIE-SQTCASDYLLFTS----SSDQYGPYCG-SMTV Local Similarity Conservative 25.8%; Score 786.5; 35.9%; Pred. No. 1. 94; Mismatches 164; pdels KELLLNTSEVTV 177 81; Gaps 16;

Sequence

669 AA

178 RFESGSHISGRGFLLTYASSDHPDLITCLERASHYLKTEYSKFCPAGCRDV 62 lfmsgihvsgrgflasysvidkqdlitcldtasnflepefskycpagcllpfak N gervrikfgdfdiedsdschfnylriyngigvsrteigkycglglqmnh eskgneitl 61 GDISGNMV 237 isgtip 121

238 DGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRYEGILANGVLSRDGSLSDKRFLF 297

Query Match

11.6%;

Score 353.5;

В 21;

Length 889;

당 Ş 밁 Qγ

1.9e-61; DB 21 Length 669; Sequence represents a specifically claimed soluble neuropillin protein sequence from the present invention. comprising an amino acid sequence in which the cell membrane-penetrating region and/or the intracellular region is dealeted from a mouse-derived neuropiilin. The soluble neuropiilin can be used for the elucidation of The present invention describes a recombinant soluble neuropillin (I) Claim 5; Page 13-17; 18pp; Japanese Soluble neuropillin having a deleted cell membrane-penetrating used to diagnose human disease conditions diagnose human 889 AA;

DR DR

WPI; 20 N-PSDB;

2000-658506/64 DB; AAC60787.

PXRXT χg ŖΧ X 20 20 ξX

> 17-FEB-1999; 17-FEB-1999; 05-SEP-2000 JP2000236879-A Synthetic E C Mouse;

99JP-0038920

99JP-0038920

(KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN



Best Local Similarity

23.1%;

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                                                WPI; 1999-132446/11
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                                                                                                                                   17-JUL-1997;
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                                                                                                                                                                                                                                                                 Neurobilin, neuropilin-2; semaphorin; transmembrane protein; axon; neurone; development; cell growth; immune response; viral phinogenesis; treatment; disease; graft rejection; viral disease; oncological disease; cancer; screening; probes.
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ceptor, neuropilin-2 - used to
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SKEXEX

22-MAR-2001 AAB64627; AAB64627

(first entry)

Human secreted protein BLAST search protein SEQ ID

NO:

밁 Ş В δÃ

415 hlgialrlelfgcrvtdapcsnmlgmlsgliadtgisass\reylwsp

462

HQRIALKVELIGCQITQGNDSLVWRKTS---QSTSVSTKKEDETITRP

yvksyklevstngedwmvyrhgknh--kvfqanndatelvlnklhtplltrfirirpqtw 414

YVKSFYMNFKNNNSKWKTYKGIVNNEEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTW 446

447

357

AAB64627 RESULT 10

standard; Protein; 439

8

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329 267

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vhqeppenfqcnaplgmesgriane---

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301 dgrwtpqgsrlhgddngwtpnvdsn----keylqvdlrfltmltaiatqgaisretqkgy

356

QVHWSPGQARLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTTG--STQSNPNF 386

-----gisasstf----s

300

275

220

17;

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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       semaphyrin and a newrophilin can be potent modulators of nerve cell growth immune responsiveness, and viral pathogenesis, and can be used in the treatment and diagnosis of neurological disease, neuro-responsiveness in the treatment and diagnosis of neurological disease, neuro-responsiveness and united the presensitivity and graft-respection, and diagnosis and treatment of viral and oncological infection/diseases. The neuropilins, neuropilins-encoding nucleic acids, and unique portions also are useful in screening chemical libraries for regulators of semaphorin-mediated cell activity, and in genetic maphing as probes for related genes, as diagnostic respents for genetic, neurological, immunological and oncological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             shown to function in repulsive axon guidance. Sema III is a serveted protein that in vitro causes neumnal growth come collepse and chemograpulsion on neurites and is required in vivo
                                                                                                                                             147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           products for the diagnosis and treatment of neurological, immunological, oncological and viral diseases
               276
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                                                                                                   221
                                                                                                                                                                                          197
                                                                                                                                                                                                                                                               146 LLF----TSSSDQYGPYCGSMTVPKELLLNTSEVTVRFESGSHISGRGFLLTY-----AS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           correct sensory afferent innervation and other aspects of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reveropment.
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-----EGILANGVLSRD-GSLSDKRFTFTSNGCSRSLSFEPDGQIRASSSWQSVNESGD 328
                                                   dckydwldiwdgiphvgpligkycgtl
                                                                                       -CPAGCRDVAGDIS--GNWVDGYRNTSLLCKAAIHAGIIADELGGQISVLQRKGISRY--
                                                                                                                                 edcsknftspngtiespgfpekyphnldctftilakprmeillqfltfdlehdplqvgeg 206
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                                                                                                                                                                                                                  ieirdgdsesadllgkhcgh\-apptiissgsvlyikftsdyarggagfslryeifktgs 146
                                                                                                                                                                                                                                                                                                            cggrlnskdagyitspyppgdypshqncewvvyapepnqkivlnfnphfeiekhdckydf 87
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 351.5; DB 20,
Pred. No. 3.7e-22;
""smatches 181;
                                             tpsklrsstgilsltfhtdmavakdgfsaryyl
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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NHP-mediated pathways. Sequence 1768

BP; 539

P 370

ü 421

ç 438

Best Local Similarity Matches 1522; Conserv Query Match Best Local

86.48; 100.08; ative

0, Score 1522; Pred. No.

Mismatches

0;

BB ₽,

240

300

61

perturbing the normal function of NHP in the body. Nucleotide encoding NHP products are used to genetically engineer host or express such products in vivo. These host cells allow for the identification of compounds that bind to NHP receptors or trig ggbggaggagctgggbgatggctgtgggacacctagtgacttatcaggatagtggcacaat NHP receptors or trigger , d 22; 0 other; Indels Length 1768 0 cells constructs Gaps 419 120 359 60 ç .300 539 240 479 180 us-09-691-344a-3.rng 0 Ş õ 밁 ρy 밁 Ş 밁 Š 밁 Š 밁 δõ 밁 δã 밁 Ş 맑 밁 1200 1680 1381 1620 1201 1141 1380 1081 1320 1260 1140 1321 1261 1500 1440 961 AC NO: AAA 96736, Database: N-genery-032802 aactaagaaagaagatgagacaatcacaaaggcccatcccctcggaagaaacatccacagg gattacadaaggtaattgattcattggtgtggggcaagacaagtcaaagcaccagtgtttc ggttgt ggttdtcccccagacatggcaccagaggatagccttgaaggtggagctcattggttgcca taaktttcgggacccagtgcaaaacaatttcatccctcccatcgtggccagatatgtgcg agotgagtttaccatcagcta@gataatgagaaggagatgacacaaaagttagatctcat ggaggctcagaaaacagact ggaggctcagaaaacagaotgttggaagcagattaaatatccctttgccagacatcagtc aatggggatctttgcag aatggggatctttgcdgcctttagaaagaagaagaaaggaaggaagtccgtatggatcagc aataaacattacaa aataaacattacaacggtggctattccattggtgctccttgttgtcctggtgtttgctgg gattacaca\u00e4ggtaatgattcattggtgtggcgcaagacaagtcaaagcaccagtgtttc laagtggaagacctataaaggaattgtgaataatgaagaaaaggtgtttcagggtaactc ccccagacatggcaccagaggatagccttgaaggtggagctcattggttgcca agatgagacaatcacaaggcccatcccctcggaagaaacatccacagg ggtggctattccattggtgctccttgttgtcctggtgttttgctgg (ctttagaaagaagaagaaaggaagtccgtatggatcagc |ttggaagcagattaaatatccctttgccagacatcagtc 1379 1080 1319 1020 1739 1380 1619 1320 1559 1260 1499 1200 1439 1140 1440

gacatctaagaattatccdgggacctaccccaatcacactgtttgcgaaaagacaattac agatttaataacatgtttggaacgagctagdcattatttgaagacagaatacagcaaatt aagtatgactgttcccaaagaactcttqttgaacacaagtgaagtaaccgtccgctttga aagtatgactgttcccaaagaactcttgttgaacacaagtgaagtaaccgttccgctttga ctgtgcttctgactatcttctcttcaccagctcttcagatcaatatggtccatactgtgg agtaccaaaggggaaaagactgattctgaggttgggagatttggatatcgaatcccagac agtaccaaaggggaaaagactbattctgaggttgggagattttggatatcgaatcccagac gacatetaagaattateeegggacetaeeecaateaeaetgtttgegaaaagaeaattae 99cggaggagctgggtgatgggctgtggacacctagtgacttatcaggatagtggcacaat | tagagatacctctttattgtgcaaagctgccatccatgcaggaataattgctgatgaact ctgcccagctggttgtagagacgtagcaggagacattctgggaatatggtagatggata ctgcccagctggttgtagagacgtagcaggagacatttctgggaaatatggtagatg agatttaataacatgtttggaacgagctagcdattatttgaagacagaatacagcaaatt gagtggatcccacatttctggccggggttttttgctgacctatgcgagcagcgaccatcc ctgtgcttctgactatcttctcttcaccagctcttcagatcaatatggtccatactgtgg 659 779 480

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480 181 420 121 360

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Polynucleotide isolated from lymph node stromal cells

of. fsn

Lymph node stromal cell; fsn -/- mice; inflammatory disorder; immune system disorder; cancer; viral disorder disorder; arthritis; blood vessel growth; tumour necrosis factor disorder; arthritis; inflammatory bowel disease; fibroblast growth factor-mediated disorder;

фs Location/Qualifiers 64..1575 /*tag= a

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1020

721 960 661 900 601 840 541 780 481 720 421 660 361

781

1080

gctggagatcgatttgggggagaaaaagaaaataacaggaattaggaccacaggatctac

<u>rtggagatcgatttgggggagaaaaagaaaataacaggaattaggadcacaggatctac</u>

ggaccaaggcccatcatgggcttcgggcgacagtagcaaccaccacaaccacgagagtg

ggaccaaggcccatcatgggcttcgggcgacagtagcaacaaccachaaaccacgagagtg

840

WO200058463-A1

gcagtcggtcaatgagagtggagaccaagttcactggtctcctggccaagcccgacttca

1019

cardiac

failure;

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959 660 899

tggttgcagcagatccttgagttttgaacctgacgggcaaatcagagcttcttcctcatg tggttgcagcagatccttgagttttgaacctgacgggcaabtcagagcttcttcctcatg

gcagtcggtcaatgagagtggagaccaagttcactggtctcctggccaagcccgacttca

caatggtgttctttcgagggatggttccctgtcagacaagcgatttctgtttacctccaa caatggtgttctttcgagggatggttccctgtcagacaagcgatttctgtttacctccaa tagagatacctctttattgtgcaaagctgccatccatgcaggaataattgctgatgaact

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standard; DNA; 1871

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18-FEB-2000; 2000WO-NZ00015



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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from arthritis. Inflammatory bowel disease and cardiac failure and a fibroblast growth factor-mediated disorder. It is also useful in assays to determine biological activity, to raise antibodies, to isolate corresponding ligands or receptors, to quantify levels of protein or cognate corresponding ligand or receptors, as antiliflammatory agents, and in compositions for the treatment of skin, connective tissue and immune system diseases. The polynucleotide is useful as marker for tissue, as a chromosome marker or tags in the identification of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isolated from lymph node stromal calls of fan // mide The polymucleotides and their polympetides are useful for treating an inflammatory disorder, disorder of immune system and cancer selected from epitheliah. lymphoid, myeloid, stromal and neuronal cancers, a viral disorder. In particular HIV infection and for modulating the growth of blood was a many the first of weather that the selection and for modulating the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          growth of blood vessels. The polypeptides are useful for treating a tumour necrosis factor (TNF) mediated disorder, such as those selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptide expressed in mammalian fen -/-, Jymph node stromal cells, useful for modulating growth of blood cells, for treating inflammate and tumour necrosis factor mediated disorders, cancer and viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strachan L,
Murison JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1871 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 60-61; 75pp;
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26-AUG-1999;
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ctatgcgagcagcgaccatccagatttaataacatgtttggaacgagctagccattattt 638
                                                                      tgaagtaaccgtccgctttgagagtggatcccacatttctggccggggttttttgctgac
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DB; AAB19126.
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99US-0383586
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Pred. No. 1.
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                                                                                                                                      Claim
                                                                                                                                                    Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                  WPI; 2001-235357,
P-PSDB; AAG75450
                                                                                                                                                                                                                                                                             28-SEP-200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aggaataattgctgatgaactaggtggccagatcagtgtgcttcagcgcaaagggatcag
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                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; cDNA;
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cancer associated nucleuc acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytastatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased educates and precisivity of p by expressing in a patient's genome that affect the activity of p by expressing in a patient's genome that affect the patients own production of P. Additionally, N may be used to produce the colon cancer-associated P, by inserting the nucleic acids into a bost cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal cardinomas and cancers. AAH37196 to AAH37204

AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleuc acid molecules (N) and proteins (P), wher

3 330 3 330 4 3118 8 299.5 8 299.5 9 276.5 10 276.5 11 271.5 11 271.5 12 268 13 268 14 29.5 17 192.5 18 29.5 19 276.5 20 20 20 20 20 20 20 20 20 20 20 20 20 2	Result No. Score	Pred. No score gra and is d	Database :	Post-processing:	Minimum DB seq Maximum DB seq	Total number o	Searched:	Scoring table:	Title: Perfect score: Sequence:	Run on:	OM protein - p	
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133	133	133.5	135	136.5	137	140.5	141	141	142.5	146.5	149.5	153	155.5	156	156
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membrane type-seri	membrane-bound arg	hensin – rabbit	hypothetical prote	Ra-reactive factor	complement subcomp	paranodin - rat	CRP-ductin-alpha p	complement subcomp	neurexin IV - mous	coagulation factor	complement subcomp	procollagen I C-pr	protein-tyrosine k	intrinsic factor-B	procollagen C-endo

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F:346-655/Domain: A2-Châ'>
F:351-688/Domain: ferroxidase repeat homology <F02>
F:656-1564/Domain: 6-COBB
F:615-1437/Region: 9-residue repeats (0-X-T/N-L-S-P-D-L-S)
F:1155-1437/Region: 9-residue repeats (0-X-T/N-L-S-P-D-L-S)
F:1565-2211/Product: coagulation factor Va light chain #status predicted <VAI>F:1565-1992/Domain: A3-Ch3>
F:1572-1992/Domain: A3-Ch3>
F:1572-1992/Domain: C1-CD1>
F:1654-1752/Region: phospholipid binding #status predicted
F:1893-2045/Domain: C1-CD1>
F:1893-2045/Domain: C1-CD1>
F:1993-2046/Domain: discoidin I amino-terminal homology <DN1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 1566-1570, 'X',1572-1581, 'X',1583-1584;1673-1676, 'X',1678-1679, 'X',1681, 'X
B; Ruse, J; Kalafatis, M; Silveira, J.R.; Kung, C.; Mann, K.G.
Biochemistry 33, 13109-13116, 1994
A; Title: Determination of the disulfide bridges in factor Va heavy chain.
A; Reference number: A55979; MUID:95034740
A; Contents: annotation
A; Contents: annotation
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C:Date: 04-Mar-1993 #sequenc_ervision 28-Apr-1995 #text_change ll-Jun-1999
C:Dates ton: A4280; A36497
R:Oulsto, B. R.: Essmon, C.T.; Mann, K.G.; MacGillivray, R.T.
A:Title: The complete cDNA sequence of bovine coagulation factor V.
A:Reference number: A4580; MUD192147638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F:1-28/Domain: signal sequence status predicted <SIG>
F:29-2211/Product: coagulation factor V status predicted <AMT>
F:29-241/Product: coagulation factor Va heavy chain #status predicted <VAH>
F:29-245/Domain: Al chait
F:29-245/Domain: ferroxidase repeat homology <FOl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Description: acts as a cofactor, with calcium and phospholipid, for the factor xa p A;Pathway: blood coagulation C;Superfamily: coagulation factor V; discoidin I amino-terminal homology; ferroxidasc C;Keywords: blood coagulation; quplication; glycoprotein; phospholipid binding; plasm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Note: 566-Cys and 617-Cys were shown to have free sulfhydryls C; Comment: Factor V is activated by thrombin and partially by coagulation factor Xa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Note: sequence extracted from NCBI backbone (NCBIN:80774, NCBIP:80776)
R:Kalaifatis, N. Jenny, R. J.; Annn, K. G.
J. Biol. Chem. 265, 21580-21589, 1990
A:Title: Identification and obstacterization of a phospholipid-binding site of bovinc A;Reference number: A36497; MUID:91072354
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A. Molecule type: mRNA
A. Residues: 1-2211 <GUI>
A. Cross Teferences: GRM1440: NID:g153037; PIDN:AAA30512.1; PID:g153038
A. Cross Teferences: GRM1440: NID:g153037; PIDN:AAA30512.1; PID:g153038
A. Mole: Sequence extracted from R. G.
B. Kalafatts
J. Biol. Chem. 255, 21580-21589, 1990
F;1833-2048/Domain: discoidin I amino-terminal homology <DN1>
F;2052-2211/Domain: C2 <CC2>
F;2052-2208/Domain: discoidin I amino-terminal homology <DN2>
F;1672-2208/Domain: discoidin I amino-terminal homology <DN2>
F;167-193,248-329,499-525/Disulfide bonds: #status experimental
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Query Match 10.8%; Score 330; DB 1; Length 927; Best Local Similarity 24.2%; Pred. No. 2e-16; Matches 112; Conservative 74; Mismatches 171; Indels 106; Gaps 20; Matches 112; Conservative 74; Mismatches 171; Indels 106; Gaps 20; Oy 66 LLALLAVSAFLAÇAEELGBGCGHLTYQDSGTMYSKYPGTYPHHTVCEKTITVPKG-124 Oy 67 LIALLAVSAFLAÇAEELGBGCGHLTYQDSGTMYSKYPGTYPHHTVCEKTITVPKG-124 Oy 68 LLALLAVSAFLAÇAEELGBCGHTKTTSPSYLTSAGYPHSYPPSQRCEMLIQAPEHY 64	C:Supertmily: Xenopus A5 antigen; CIr/Cls repeat homology; discoidin I amino-terminal; C:Keywords: duplicantion; glycoprotein; transmenbrane protein F:I-Zl/Domain: signal sequence #status predicted <sig> F:Z2-29Z/Product: A5 antigen #status predicted <sig> F:Z7-138/Domain: CIr/Cls repeat homology <ciri> F:Z7-138/Domain: CIr/Cls repeat homology <ciri> F:Z74-444/Domain: discoidin I amino-terminal homology <cnn> F:Z74-444/Domain: discoidin I amino-terminal homology <cnn2> F:46-812/Domain: discoidin I amino-terminal homology <cnn2> F:561-883/Domain: transmenbrane #status predicted <tmm> F:500-261,300,523,844/Binding site: carbohydrate (Asn) (covelent) #status predicted</tmm></cnn2></cnn2></cnn></ciri></ciri></sig></sig>	C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000 C:Accession: JH0465, J09948 R:Takagi, S: Hirata, T: Agata, K: Mochil, M.; Eguchi, G.; Fujisawa, H. Neuron 7, 295-207, 1991 Neuron 7, 295-207, 1992	Oy 431 IPPIVARYVRVPOTWHORIALKVELIGGOI 461 :: :: : : : Db 2180 NPPIISRFIRIIFKTWNQSIALRLEIFGCDM 2210 RESULT 2 J00948 A5 antigen precursor - African clawed frog C.Species: Kenopus laevis (African clawed frog)	Db 2026	Query Match 10.8%; Score 331; DB 1; Length 2211; Best Local Similarity 32.5%; Pred. No. 6.1e-16; Matches 88; Conservative 48; Mismatches 89; Indels 46; Gaps 10; Qy 209 ASHYLKTEY-SKFCPAGCRDVAGDISGNMYDGYRDTSLICKAAIHAGIIADE 259	F:225,239,297,382,460,553,587,745,756,774,780,902,952,964,1044,1053,1062,1071,1078,1094, F:334-335/Cleavage site: Arg-Asn (protein C) #status predicted F:356,597,1537/Binding site: snifate (Tyr) (covalent) *status predicted F:356,957,1537/Binding site: snifate (Tyr) (covalent) *status predicted F:356,397,1537/Binding site: Arg-Giy (protein C) #status predicted F:607-88,1712-1718,194-2048,055-2208/Disnlifide bonds: #status predicted F:741-742/Cleavage site: Arg-Ser (cosquiation factor Xa, thrombin) *status predicted F:7104-1035/Cleavage site: Arg-Ser (cosquiation factor Xa, thrombin) *status predicted F:104-1035/Cleavage site: Arg-Ser (cosquiation factor Xa, thrombin) *status predicted F:1564-1565/Cleavage site: Arg-Ser (thrombin) *status experimental*
A; Cross-reterences: us:M.//80 A;Note: parts of this sequence were determined by protein sequencing R;Kane, W.H.; Davie, E.M. Proc. Natl. Acad. Sci. U.S. A. 83, 6800-6804, 1996 A;Title: Cloning of a cDNA coding for human factor v, a blood coagulation factor homo A;Reference number: A25897; MJID:86313665 A;Accession: A25897 A;Molecule type: mRNA	A,Accession: A28028 A,Molecule type: mm,NB59-864,'R',856-924,'E',926-1763,'I',1765-2212,'T',2214-2224 <j 1-1284,'i',1286-1600="" 1-857,'r',856-924,'e',926-1763,'i',1765-2212,'t',2214-2224="" 1987="" 26,="" 6508-6514,="" <j="" <kan="" a,note:="" a,residues:="" a,tille:="" a.;="" a27498="" a27498;="" a;accession:="" a;cross-references:="" a;molecule="" a;reference="" a;residues:="" amino="" and="" biochemistry="" cdnas="" chain="" cloning="" coding="" connecting="" d="" davie,="" e.w.="" end="" f.s.;="" for="" gb:m16567="" hagen,="" heavy="" ichinose,="" including="" mature="" mmaa="" muid:88107560="" number:="" of="" parts="" protein,="" r;kane,="" region="" sequence,="" the="" this="" type:="" w.h;="" were=""> A;Residues: 1-1284,'I',1286-1600 <kan></kan></j>	8 239-249;313-323;368 ; Kriz, R.W.; Alda 850, 1987 acid sequence of h	RESULT 3 KRHU5 Coagulation factor V precursor [validated] - human N; Alternate names: coagulation labile factor; proaccelerin N; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 19-May-1989 #sequence_revision 02-Jun-1995 #text_change 08-Dec-2000 C; Accession: A55172: A43344; A2802B; A27498; A27897 R; Cripe, L.D.; Moore, K.D.; Kane, W.H. Blochemistry 31, 3777-3785, 1992 A; Title: Structure of the gene for human coagulation factor V.	OP A PARESCELLE UNIT SOME SENSON SERVICE VERWINDER FOR A SENSON S	200	125 65 180

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c:Species: Mus musculus (house mouse)
C:Date: 11-1an-2000 #sequence_revision
C:Accession: T42764
E:Yang, T.L.; Cul; J.; Rehumtulla, A.;
Blood 91, 4593-4599, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #:2065-2221/Domain: discoidin I amino-terminal homology <DN2>
#:51,55,239,297,460,466,554,741,752,766,776,782,881,983,977,1074,1083,1103,1106,1479,149
#:167-193,248-729,500-526,603-664,1725-1751,1907-2061,2066-2221/Disulfide bonds: #status
#:347-335/Cleavage site: Arg-Asn (protein C) #status predicted
#:343-335/Cleavage site: Arg-Ser (coagulation factor Xa) #status predicted
#:346-377/Cleavage site: Arg-Ser (coagulation factor Xa) #status bredicted
#:382,1339/Binding site: carbohydrate (Asn) (covalent) #status absent
#:544-335/Cleavage site: Arg-Ser (coagulation factor Xa, thrombin) #status experimental
#:737-738/Cleavage site: Arg-Thr (coagulation factor Xa, thrombin) #status experimental
#:1046-1047/Cleavage site: Arg-Ser (thrombin) #status experimental
#:1046-1047/Cleavage site: Arg-Ser (thrombin) #status experimental
                                                                                                                                                                     coagulation
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F:1567-1765/Region: phosphoilpid binding #status predicted
F:1906-2064/Domain: C1 <BC15-
F:1906-2064/Domain: C1 <BC15-
F:1906-2064/Domain: C2 <BC25-
F:2065-2224/Domain: C2 <BC25-
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F;351-884/Domain: ferroxidase repeat homology <F02>
F;692-1573/Domain: B <DOB>
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F:29-2224/Product: coagulation factor V *status predicted <MAT>
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A;Cross-references: GB:M14335
Biochemistry 34, 4118-4124, 1995
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F;1574-2224/Product: coagulation factor Va light chain #status experimental <VAL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Contents: annotation; thrombin cleavage sites C; Comment: Factor V is activated by thrombin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: A56139; MUID:95210278
A;Contents: annotation; thrombin cleavage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
T.L.; Cui, J.; Rehumtulla, A.; Yang, A.; Moussalli, M.; Kaufman, R.J.;
11, 4593-4599, 1998
                                                                                                                                                                                                                                                                                                                                     DKIFEGNTNTKGHVKNEFNPPIISRFIRVIPKTWNQSIALRLELFGCDI 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NNHKPREWLEIDLGEKKKITGIRTTGSTQSNFNFYVKSFVMNFKNNNSKWKTYKGIVNNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NGCSTPLGMENGKIENKQITASSFKKSWW-----GD--YWEPFRARLNAQGRVNAWQAKA 2116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNNK--QWLEIDLLKIKKITAIITQGCKSLSSEMYVKSYTIHYSEQGVEWKPYRLKSSMV
                                                                                                                                                                         factor V - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ferroxidase repeat homology <FO1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 321; DB 1;
Pred. No. 3.5e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                         11-Jan-2000 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant human factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             466/1; 537/3; 588/1; 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     412
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A.Title: The structure and function of murine factor V and its inactivation by prote A.Reference number: 22277; MUID:98282202
A.Roccession: 742764
A.Status: preliminary; translated from GB/EMBI/DDBJ
A.Kolecule type: mRNA
A.Rosiduss: 1-2183 <ANN
A.Rosiduss: 1-2183 <ANN
A.Rosiduss: 1-2183 <ANN
A.Gross-references: EMBI:U52925; NID:g3219690; PID:g3219691; PIDN:AAC99553.1
C.Function:
A.Fathway: blood coagulation
C.Superfamily: coagulation factor V; discoidin I amino-terminal homology; ferroxidase C.Keywords: blood coagulation; duplication; glycoprotein; phospholipid binding; plass F; 350-682/Domain: ferroxidase repeat homology cFOXI>
F; 350-682/Domain: ferroxidase repeat homology cFOXI>
F; 1541-1864/Domain: ferroxidase repeat homology cFOXI>
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Matches
                                                                                                                                                                                                                                                                                    Query Match
Best Local
2134 DKIFEGNSNTKGHMKNFFNPPIISRFIRIIPKTWNQSIALRLELFGCDI 2182
                                                                                                                                                                       2023 NGCSTPLGLEDGRIQDKQITASSFKKSWW-----GD--YWEPSLARLNAQGRYNAWQAKA 2075
                                      413 EKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGCQI 461
                                                                                                                              353 NNHKPREWLEIDLGEKKKITGIRTTGSTQSNFNFYVKSFVMNFKNNNSKWKTYKGIVNNE 412
                                                                                                                                                                                                                   300 NGCSRSLSFE----PDGQIRASS---SWQSVNESGDQVHWSPGQARLQDQGPSWASGDSS
                                                                                  NNNK--QWLQVDLLKIKKVTAIVTQGCKSLSSEMYVKSYSIQYSDQGVAWKPYRQKSSMV
                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                 10.4%;
                                                                                                                                                                                                                                                            31;
                                                                                                                                                                                                                                                                                 Score 318; DB 2;
Pred. No. 5.7e-15;
                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                     Length 2183;
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                      352
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MSJULY 3
A47285
A47285
A47285
C;Bpecies: Homo sapisms (man)
C;Bpecies: Homo sapisms (man)
C;Bpecies: J1-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 28-May-1999
C;Accession: A47285
R;Larocca, D.; Peterson, J.A.; Urree, R.; Kuniyoshi, J.; Bistrain, A.M.; Ceriani, R.[
Cancer Res. 51, 4944-998, 1991
A;Pitle: A.M-r 65,000 human milk fat globule protein that is highly expressed in human A;Reference number: A47285; MUID:91371351
A;Roccession: A47285; MUID:91371351
A;Roccession: A47285; MUID:91371351
A;Caccession: A47285; MUID:91371351
A;Caccession: A47285; MUID:9137359; PIDN:AAB19771.1; PID:9235397
A;Molecule type: mRNA
A;Rosidues: 1-218 < CLARA;Caccession: A47285; MUID:9235396; PIDN:AAB19771.1; PID:9235397
A;Cross-references: Gis:556151; NID:9235396; PIDN:AAB19771.1; PID:9

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JC4915
ags protein precursor - rat
N;Alternate names: O-acetyl-Gd3 ganglioside
                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                              351
                                                                                                                                        411 NEEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGC 459
                                                                                                                                                                            114
                                                                                                                                                                                                                                                                            300 NGCSRSLSFE----PDGQIRASSSWQSVNESGDQVH---WSPGQARLQDQG--PSWASGD 350
                                                                                                                                                                                                                                            59 NGCANPLGLKNNSIPDKQITASSSYKTWG-----LHLFSWNPSYARLDKQGNFNAWVAGS
                                                                                                                                                                          YGND----QWLQVDLGSSKEVTGIITQGARNFGSVQFVASYKVAYSNDSANWTEYQDPRT
                                                                                                                                                                                                            SSNNHKPREWLEIDLGEKKKITGIRTTGSTQSNFNFYVKSFVMNFKNNNSKWKTYKGIVN
                                                                                                        GSSKIFPGNWDNHSHKKNLFETPILARYVRILPVAWHNRIALRLELLGC
                                                                                                                                                                                                                                                                                                                63;
                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                             9.8%;
                                                                                                                                                                                                                                                                                                              33;
                                                                                                                                                                                                                                                                                                                                Score 299;
Pred. No.
                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                             Length 218
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                                                                                                        218
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                                                                                                                                                                            169
                                                                                                                                                                                                                                            113
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Tesdues: 1-1921.'S',1923-2351 <RES>
Tross-references: GB:M88648; NID:9187381; PrDN:AAA52420.1; PTD:9182383
Tross-references: GB:M88648; NID:9187381; PrDN:AAA52420.1; PTD:9182383
Tross-references: GB:M88648; NID:9187381; PrDN:AAA52420.1; PTD:9182383
Ture 312, 330-337, 1984
Ture 312, 330-337, 1984
Tesference number: A00525; MUID:85061548
Turess-references: EMBL:X01165; EMBL:X01166; EMBL:X01179
Tess-references: EMBL:X01165; EMBL:X01166; EMBL:X01179
Tess-references: EMBL:X01165; EMBL:X01166; EMBL:X01179

Nolecule type: mRNA Molecules; 1-251 4005 Cross-references: EMBL:X01165; EMBL:X01166; EMBL:X01179 Toole, J.J.; Knopf, J.L.; Wozney, J.M.; Sultzman, L.A.; Buecker, J.L.; Pittman, D.D. D.N.; Hewick, R.M. ture 312, 342-347, 1984 Title: Molecular cloning of a cDNA encoding human antihaemophilic factor. Reference number: 158059; MUID:85061550 Accession: T58059 Accession: T58059

Liecule type: mRNA. sides: 1-74. 'V',76-1259,'E',1261-2351 <RE2> sidues: 1-74. 'V',76-1259,'E',1261-2351 <RE2> oss-references: GB:K01740; NID:g182802; PIDN:AAA52484.1; PID:g182803 oss-references: GB:K01740; NID:g182802; PIDN:AAA52484.1; PID:g182803 oss-references: GB:K01740; NID:g182802; PID:AAA52484.1; PID:g182803 oss-references: GB:K01740; PID:g182803; NID:g182802; PID:AAA52484.1; PID:g182803; NID:g182802; PID:AA52484.1; PID:g182803; NID:g182803; NID:g182803; NID:g182802; PID:AA52484.1; PID:g182803; NID:g182803; NI

ccession: A23584
lecule type: mRNA
sidues: 1-2351 CTRU>
cos-references: GB:M14113; NID:g182817; PIDN:AAA52485.1; PID:g182818
toos. D.; Rodriguez, H.; Vehar, G.A.
themistry 25, 505-512, 1986

A; Title: Proteolytic processing of human factor VIII. Correlation of specific cleavagity for the proteon of the proteon of specific cleavagity for the proteon of the prot

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F:7716-2039/Domain: ferroxidase repeat homology <PO3>
F:0139-2181/Domain: discoldin I amino-terminal homology <PON1>
F:2039-2181/Domain: discoldin I amino-terminal homology <PON1>
F:2039-2181/Domain: discoldin I amino-terminal homology <PON2>
F:2139-2331/Domain: discoldin I amino-terminal homology <PON2>
F:2139-2331/Domain: discoldin I amino-terminal homology <PON2>
F:2139-2331/Domain: discoldin I amino-terminal homology <PON2>
F:2039-2331/Domain: discoldin I amino-t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Keywords: acute phase; blood coagulation; duplication; glycoprotein; hemophilia F:1-19/Domain: signal sequence #status predicted CSIG-F:10-2351/product: coagulation factor VIII #status experimental CMATS-F:20-740/Product: coagulation factor VIIIa heavy chain #status experimental CMCHS-F:20-740/Product: coagulation factor VIIIa heavy chain factor VIIIa heavy chain factor VIIIa heavy chain factor VIIIa 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Pathway: blood coagulation
C; Superfamily: coagulation factor VIII; discoidin I amino-terminal
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A:Cross-references: GDB:119124; OMIM:306700
A:Map position: Xq28-Xq28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 1668-1685 <LIN>C; Comment: Factor VIII is a
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Lind, P.; Larsson, K.; Sp. 1945, Sydow-Baeckman, M.; Almstedt, A.; Gray, E.; Sandberg Eur. J. Blochem, 232, 19-27, 1998
Eur. J. Blochem, 232, 19-27, 1998
A; Title: Novel forms of B-domain-deleted recombinant factor VIII molecules. Construction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 733-752; 753-759 < KJA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Contents: annotation; disulfide bonds
A:Rote: 329-(79; 711-(79; and 20)9-(79; were shown
R:Njalko, M.; Heding, A.; 7albo, 199; Persson, B.;
Eur. J. Biochem. 234, 73:779, 1995
A:Title: Amino acid residues 72:17-29 are required
A:Reference number: $65527; MUID:96163459
A:Accession: $63527
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R.McMullen, B.A.; Bujtkawa, K.; Davie, E.W.; Hedner, U.;
Protein Sci. 4, 740-746, 195
A.Title: Locations of disulfide bonds and free cystoines
A.Reference number: A56216; MUID:95338127
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R;Coltschier, J.; Wood, W.I.; Goralka, T.M.; Wion, K.L.;
Nature 312, 326-330, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol. Chem. 266, 740-746, 1991
A:Title: Sulfation of Tyr(1680) of human blood
A:Reference number: A56109; MUID:91093266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Molecule type: protein
A; Mestdues: "X', 517-523;1853-1860, 'X',1862-1864, 'X',1866 <FA:
R; Leyte, A.; van_Schijndel, H.B.; Niehrs, C.; Huttner, W.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 20-36;356-371;392-408;582-594;1668-1669, 'X',1671;1672-1692;1693-1708;1709-17-48; Experimental source: recombinant material from Chinese hamster ovary cells A; Note: sequence extracted from NCBI backbone and corrected to correspond with the publi R; Fay, P.J.; Smidzin, T.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;1709-2038/Domain: A3 <DA3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;1668-2351/Product: coagulation factor VIIIa light chain
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F;760-1667/Domain: B <DB0>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;23-348/Domain: ferroxida: F;392-759/Domain: A2 <DA2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Introns: 48/2; C; Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chem. 264, 14005-14010, 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acts as a cofactor, with calcium and phospholipid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ferroxidase repeat homology <FO1>
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Thomsen,
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Ezban, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     experimental <ACL>
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ein; hemophilia
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Best Local
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F:414.45/Binding site: sulfate (Tyr) (covalent) #status predicted F:759-760/Cleavage site: Arg-Ser (coagulation factor Xa. thrombin) #status experiment F:1667-1668/Cleavage site: Arg-Ser (coagulation factor Xa. thrombin) #status experimental F:1708-1709/Cleavage site: Arg-Ser (coagulation factor Xa. thrombin) #status experime F:1708-1709/Cleavage site: Arg-Nat (coagulation factor Xa) #status experimental F:1708-1740-1741/Cleavage site: Arg-Nat (coagulation factor Xa) #status experimental F:1708-1741/Cleavage site: Arg-Na
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Best Local
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KPREWLEIDLGEKKKITGIRTTGSTQSNFNFYVKSFVMNFKNNNSKWKTYKGIVNNEEKV 415
                                                                                                                                                        NSCSMPLGMESKAISDAQITASSYFTNMFAT----WSPSKARLHLQGRSNAWRPQVNN-
                                                                                                                                                                                                                                                                                            NGCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSNNH
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Pred. No. 1.
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1.7e-12;
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FQGNQDSFTPVVNSLDPPLLTRYLRIHPQSWVHQIALRMEVLGCE 2346 FQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGCQ

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F:68-107/Domain: EGF homology <EG2>
F:147-303/Domain: discoidin I amino-terminal F:307-463/Domain: discoidin I amino-terminal
                                                                                                                                                                    C; Keywords: membrane protein F; 28-60/Domain: EGF homology <EG1>
                                                                                                                                                                                                                 A;Cross-references: GB:M38337; NID:g199142; PIDN:AAA39534.1; PID:g199143 C;Superfamily: milk fat globule protein; discoidin I amino-terminal homology;
                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-463 <STU>
                                                                                                                                                                                                                                                                                                                                     A; Reference number:
A; Accession: A36479
                                                                                                                                                                                                                                                                                                                                                              R;Stubbs, J.D.; Lekutis, C.; Singer, K.L.; Bui, A.; Yuzuki, D.; Srinivasan, U.; F
Proc. Natl. Acad. Sci. U.S.A. 87, 8417-8421, 1990
A;Title: cDNA cloning of a mouse mammary epithelial cell surface protein reveals
A;Reference number: A36479; MUID:91046008
                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Stubbs, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Species:
                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fat globule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A36479
9.18;
Score 276.5;
Pred. No. 7.
                                                                                             homology
homology
                         DB 1;
                      Length
                         463
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305 234 115

NLDGEYMFTTAVPNTAVPTPAPTPDLSNNLASRCSTQLGMEGGAIADSQISASYVYMGFM

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TGLVCNETERGPCSPNPCYNDAKCLVT-LDTQRGDIFTEYICQCPVGYSGIHCETETNYY

------SDHPDLITCLERASHYLKTEYSKFCPAGCRDVAGDISGNM-

236 55

237

-VDG-YRDTSLLCKAAI----

259

---ELGGQISVLQRKGI--

-----SLSDKRFLFTSN--

GLQRWGPELARLYRTGIVNAWHASNYDSKPWIQVNLLRKMRVSGVMTQGA-SRAGRAEYL

SRYEGILANGVLSRDG-----

174

258

----GCSR-

233 288

KTFKVAYSLDGRKFEFIQDESGGDKEFLGNLDNNSLKVNMFNPTLEAQYIRLYPVSCHRG

PDGQIRASSSWQSVNESGDQVHWSPGQARLQDQG

343

293 304 191

56

141 CASDYLLFTSSSDQYGPYCGSMTVPKELLLNTSEVTVRFESGSHISGR--

112;

Conservative

59;

Mismatches

118;

Indels

189;

Gaps

21;

190

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Similarity

16 CASG--LFAASGD----FCDS----SLCLN------GGTCLTGQDNDIYCLCPEGF

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coapulation factor VIII precursor - plg
c;Species: Sus scroia domestica (domestic pig)
c;Species: Il-dan-2000 #sequence_revision 11-dan-2000 #text_change 09-Jun-2000
C;Datus: Il-dan-2000 #sequence_revision 11-dan-2000 #text_change 09-Jun-2000
C;Accession: 742763
R;Collar P
submitted to the EMBL Data Library, August 1996
A;Reference number: 22269
A;Accession: 742763
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-213 < COL>
A;Rectendily: coasulation factor VIII discoldin I amino-terminal homology; ferroxida
C;Reywords: acute phase; blood coagulation, duplication; diyplostion; place phase; blood coagulation, duplication; glycoprotein; hemophilia A; p
F;10-2133/Product: coagulation factor VIII #status predicted <ANT>
F;20-313/Product: coagulation factor VIII #status predicted <ANT>
F;21-39/Commain: ferroxidase repeat homology <FOXI>
F;21-39/Commin : ferroxidase repeat homology <FOXI>
F;21-39/Commin : ferroxidase repeat homology <FOXI>
F;420-30/Commain: ferroxidase repeat homology <FOXI>

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C;Species: Mus musculus (house mouse)
C;Accession: A4704 #sequence_revision 09-Sep-1994 #text_change 18-Jun-1999
C;Accession: A4704
R;Elder, B; Lakich, D; Gitschier, J.
Genomics 16, 374-379, 1993
A;Title: Sequence of the murine factor VIII cDNA.
A:Reference number: A4704; MUID:93300511
A;Accession: A4704
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2319 <a href="https://doi.org/10.1005/19.100573">https://doi.org/10.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005/19.1005
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352 KINAW----TAQSNSAKEWLQVDLGTQRQVTGIITQGARDFGHTQYVESYKVAHSDDGVQ 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     344 P--SWASGDSSNNHKPREWLEIDLGEKKKITGIRTTGSTQSNFNFYVKSFVMNFKNNNSK 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGCQITQ 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -PKQWLQVDLQKTMKVTGIITQGVKSLFTSMFVKEFLISSSQDGHHWTQI--LYNGKVKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KPREWLEIDLGEKKKITGIRTTGSTOSNENEYVKSFYMNFKNNNSKWKTYKGIVNNEEKV 415
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Pred. No. 8.1e-12;
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                                                                                                                                                                                                                                               amino-terminal homology; ferroxidas
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Best Local
                                                                         2021
                                                                                                                                                1973 NSCSMPLGMQNKAISDSQITASSHLSNIFAT----WSPSQARLHLQG-----RTNAW 2020
2079 GHTKVFQGNQDSSTPVVNALDPPLFTRYLRIHPTSWAQHIALRLEVLGCE 2128
                                                                                                             356
                                   411 NEEKVFOGNSNERDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGCQ 460
                                                                                                                                                                                    300 NGCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSNNH 355
                                                                                                                                                                                                                                            Local Similarity
                                                                         RPRVSSAEEWLQVDLQKTVKVTGITTQGVKSLLSSMYVKEFLVSSSQDGRRWTLF--LQD
                                                                                                          KPR-----EWLEIDLGEKKKITGIRTTGSTQSNFNFYVKSFVMNFKNNNSKWKTYKGIVN 410
                                                                                                                                                                                                                             61
                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                       35.98;
                                                                                                                                                                                                                          29;
                                                                                                                                                                                                                                            Score 271.5; DB:
Pred. No. 1.7e-11;
                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                          57;
                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                2133;
                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                        Gaps
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C; Superfamily: milk fat globule protein; discoldin C; Reywords: glycoprotein C; Reywords: glycoprotein (fragment) < EG1>
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R;Aokl, N.; Kishi, M.; Taniguchi, Y.; Adachi, T.; Nakamura, R.; Matsuda, T.
Biochim, Blophys. Acta 1245, 385-391, 1995
A;Title: Molecular cloning of glycoprotein antigens MGP57/53 recognized by monoclonal A;Beference number: 865138; MUID:96125736
A;Accession: 865138
F;82-239/Domain: discoidin I amino-terminal homology F;82-239/Domain: discoidin I amino-terminal homology
                                                                                                                                                                                                                                                                                        A;Reference number: A48394; MUID:93250576
A;Accession: G48394
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Mol. Biol. Int. 29, 54
A; Title: The major fat-globule
                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Mather, I.H.; Banghart,
Biochem. Mol. Biol. Int. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycoprotein antigen MGP57/53, mammary gland - bowine (fragment)
N:Alternate names: glycoprotein component 16/major fat-globule membrane protein/NFG-E
C:Species: Bos prinigenius taurus (cattle)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 07-Aug-1998
                                                                                                                                                                               A; Note: sequence extracted from NCBI backbone (NCBIP:131457)
                                                                                                                                                                                                          A; Experimental source: milk
                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 207-220 <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; not compared with conceptual
                                                                                                                                                                                                                                                                                                                                                                                  II-like sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1-401 <AOK>
                                                                                                                                                                                                                                                                                                                                                                                                                                             L.R.; Lane,
29, 545-554,
                                                                                                                                                                                                                                                                                                                                                                                                              membrane proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                             W.S.
                                                                                                                                                                                                                                                                                                                                                                                                                 bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation
                                       CING>
                                                                                                                                                amino-terminal homology; EGF
           <DN2:
                                                                                                                                                                                                                                                                                                                                                                                                              components 15/16
                                                                                                                                                                                                                                                                                                                                                                                                                 and
                                                                                                                                                                                                                                                                                                                                                                                                                 guinea-
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354 NHKPREWLEIDLGEKKKITGIRTTGSTQSNENFYVKSFVMNFKNNNSKWKTYKGIVNNEE 413

S----EWLQIDLGSQKRVTGIITQGARDFGHIQYVAAYRVAYGDDGVTWTEYKDPGASES

459 401

300 NGCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWSPGQARLQDQGP--SWASGDSSN 353

NGCTEPLGLKDNTIPNKQITASSYYKTWGLSA--FSWFPYYARLDNQGKFNAWTAQTNSA 299

242

Local Similarity

8.8%;

Score 268; DB 2; Pred. No. 2.6e-12

Length 401

61;

Conservative

30;

Mismatches

63;

Indels

12; Caps

4

356 KIFPGNMDNNSHKKNIFETPFQARFVRIQPVAWHNRITLRVELLGC 414 KVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGC

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A;Experimental source: testis
C;Function:
A;Description: may be involved in membrane remodeling and/or function as a zona
C:Superfamily: unassigned EGF-related proteins; EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F:24-89/Domain: BGF homology <BG1>
F:66-105/Domain: BGF homology <BG2>
F:66-105/Domain: BGF homology <BG2>
F:108-265/Domain: BGF homology <BG2>
F:108-265/Domain: discoidin I amino-terminal homology <DNI>
F:249-427/Domain: discoidin I amino-terminal homology <DNI>
F:24-527/Binding site: carbohydrate (Ser) (covalent) #status experimental F:34/Binding site: carbohydrate (Ser) (covalent) #status experimental F:59/Binding site: carbohydrate (Ann) (covalent) #status experimental F:59,227/Binding site: carbohydrate (Ann) (covalent) #status experimental F:59,227/Binding site: carbohydrate (Ann) (covalent) #status experimental F:59-227/Binding site: carbohydrate (Ann) (covalent) #status experimental
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A;Molecule type: protein
R;Kim, D.H.; Kanno, C.; Mizokani, Y.
Blochim. Blophys. Acta 1122, 203-211, 1992
Blochim. Blophys. Acta 1122, 203-211, 1992
A;Title: Purification and characterization of major glycoproteins, PAS-6 and PAS-7, from A;Reference number: 823926; MOID:92353107
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C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 20-Jun-2000
C;Accession: 574211: 578114; 524181
E;Hvarregaard, J.; Andersen, M.H.; Berglund, L.; Rasmussen, J.T.; Petersen, Eur. J. Biochem. 240, 628-630, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAS-6/7 protein precursor - bovine C; Species: Bos priming:
                                                                                                   A; Molecule type: mRNA
A; Residues: 1-409 <ENS>
A; Cross-references: EMB
                                                                                                                                                                                                                       A:Title: Molecular cloning and characterization of P47, A:Reference number: Z17325; MUID:98206817
                                                                                                                                                                                                                                                                       R;Ensslin, M.; Vogel, T.; Calvete, J.J.; Thole, H.H.; Schmidtke, Biol. Reprod. 58, 1057-1064, 1998
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                                                                                                                                                                          A; Status: preliminary; translated
                                                                                                                                                                                                       A; Accession: T11743
                                                                                                                                                                                                                                                                                                                          C; Accession: Tl1743
                                                                                                                                                                                                                                                                                                                                              C;Date: 16-Jul-1999 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                              pP47 protein
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A; Residues: 383-394 < KIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S24181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S78114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X91895; NID:g1632778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-427 <HVA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S74211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Characterization of glycoprotein PAS-6/7 A; Reference number: S74211; MUID:97008954
                                                                                                                                                                                                                                                                                                                 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S----EWLQIDLGSQKRVTGIITQGARDFGHIQYVAAYRVAYGDDGVTWTEYKDPGASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NHKPREWLEIDLGEKKKITGIRTTGSTOSNENFYVKSFVMNFKNNNSKWKTYKGIVNNEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGCTEPLGLKDNTIPNKQITASSYYKTWGLSA--FSWFPYYARLDNQGKFNAWTAQTNSA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWSPGQARLQDQGP--SWASGDSSN'353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                   EMBL: Y11683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30;
                                                                                                   NID:g2652927; PIDN:CAA72379.1; PID:g2652928
                                                                                                                                                                          from GB/EMBL/DDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 268; DB 2;
Pred. No. 2.9e-12;
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                                                                                                                                                                                                                                                                                             J.; Matsuda,
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F; 6-40/Domain: EGF homology <EGF>
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Matches
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                                                                                                                                                                                                                                                           291
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                                                                                                                                                                                                                                                                                                                                                                  72 TEYICKCPHGYTGIHCEIICNAPLGMETGAIADFQISASSMHLGFMGLQRWAPELARLHR_131
EGKIFPGNLDNNSHKKNMFETPFLTRFVRILPVAWHNRITLRVELLGC
                                    EEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGC
                                                                                                           SNNHKPREWLEIDLGEKKKITGIRTTGSTQSNFNFYVKSFVMNFKNNNSKWKTYKGIVNN
                                                                                                                                                ELSGCAEPLGLKDNTIPNKQITASSFYRTWGLSA~~FSWYPFYARLDNQGKFNAWTAQSN
                                                                                                                                                                                    SRSLSFEPDG-----
                                                                                                                                                                                                                                                                                                AGIVNAWTASNYDRNPWIQVNLLRR----MRVTGVVTQGA-SRAGSAEYMKTFKVAYSTDG
                                                                                                                                                                                                                         RKFQFIQGAEESGDKIFMGNLDNSGLKVNLFEVPLEVQYVRLVPIICHRGCTLRFELLGC
                                                                                                                                                                                                                                                             ------SDKRFL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                             87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                         EWLQIDLGSQRRVTGIITQGARDFGHIQYVAAYKVAYSDDGVSWTEYRDQGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.5%;
25.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 259.5; DB 2
Pred. No. 1.2e-11;
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Biochem. Biophys. Res. Commun. 228, 411-414, 1996
A;Title: A CDNA cloning of human AEBPI from primary cultured
A;Reference number: JC2256; MUID:97079196
A;Cross-references: DDBJ:D86479; NID:g1468942; PIDN:BAA13094.1; PID:g1468943
                                  A; Molecule type: mRNA
A; Residues: 1-845 <OHN>
                                                                                                                               A; Accession:
                                                                                                                                                                                                                                                           C; Accession: JC5256
R; Ohno, I.; Hashimoto, J.; Shimizu, K.; Takaoka, K.; Ochi, T.; Matsubara, K.;
                                                                                                                                                                                                                                                                                                                      C; Species: Homo sapiens (man)
C; Date: 16-Jul-1999 #sequence
                                                                                                                                                                                                                                                                                                                                                                                      adipocyte transcription factor, AEBP1 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                          15
                                                                                                 preliminary
                                                                                                                                        JC5256
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                                                                                                                                                                                               osteoblasts and its exp
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311 DGQIRASSSWQ-SVNESGDQVHWSPGQARLQDQGPSWASGDSSNNHKPREWLEIDLGEKK

84

Local

55; Similarity

Conservative

40;

Score 217; DB Pred. No. 5.3e 40; Mismatches

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Length 845;

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Indels

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7.1%;

Search completed: July Job time: 3801 sec 9 2002, 02:16:44

258 475 198 430 140 370

QSTSVSTKKEDETITRPIPSEETSTGINITTVAI 508

ROLMKVVNEECPTITRTYSLGKSSRGLKIYAMEI

29

LPEPVVARFIRIYPLTWNGSLCMRLEVLGCSVAPVYSYYAQNEVVATDDLDFRHHSYKDM 257

FIPPIVARYVRVVPQTWHQRIALKVELIGCQITQ----

-- GNDSLVWR----KTS

RETGVITQGRDSSIHDDFVTTFFVGFSNDSQTWVMYTN--GYEEMTFHGNVDKDTPVLSE 197 KITGIRTTGSTQSNFNFYVKSFVMNFKNNNSKWKTYKGIVNNEEKVFQGNSNFRDPVQNN DNQIRASSMLRHGLGAQRGRLNMQTGATEDDYYDGAWCAEDDART----QWIEVDTRRTT 139

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Result
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Maximum Match 100%
Listing first 45 summaries
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         Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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CTA4_HOUSE
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58	NRP2_RAT STANDARD; PRT; 925 AA.	
Ę ĉ	053270; 16-0CT-2001 (Rel. 40, Created)	
Ŋ	(Rel. 40,	
Ŋ	16-OCT-2001 (Rel. 40, Last annotation update)	
DE	precursor	
DE	receptor 2).	
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გ	data;	
8	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
ò	NCBI_TaxID=10116;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-SPRAGUE-DAWLEY;	
RX	MEDLINE-97433085; PubMed-9288754;	
R	Kolodkin A.L., Levengood D.V., Rowe E.G., Tai.YT., Giger R.J.,	
RA	Ginty D.D.;	
RT.	"Neuropilin is a semaphorin III receptor ";	
RL	1 90:753-762(1997).	
S	-1- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORING 3C, 3F, VEGF-165	
ဂ္ဂ	AND VEGE-145 ISOFORMS OF VEGE, AND THE PLGE-2 ISOFORM OF PGF.	
8	-!- SUBCELLULAR LOCATION: Type I membrane protein.	
S	-!- TISSUE SPECIFICITY: FOUND IN CERTAIN NEURONAL POPULATIONS OF THE	
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C	-!- SIMILARITY: CONTAINS & F3/6 TIPE C DOMAINS.	
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S	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
8	the European Bioinformatics Institute. There are no restrictions on its	٠,
18	use by non-profit institutions as long as its content is in no way	_
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EMBL, AP016297; AAC53338.1; ...
InterPro; IPR000859; CUB.
InterPro; IPR000421; EA58.C.
InterPro; IPR000939; AAM.
Pfam; PP00731; CUB; 2.
Pfam; PP00731; CUB; 1.
Pfam; PP00734; F_FE_LTPC_C; 2.

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SMART; SMO031; FASE; 2.
SMART; SMO0137; MAM; 1.
PROSITE; PS011100; CUB: 2.
PROSITE; PS01285; FASE(_2; 2.
PROSITE; PS01285; FASE(_2; 2.
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PROSITE; PS01285; FASE(_2; 2.
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Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor 22

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050452; 0.14820; 0.14821;
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16-0CT-2001 (Rel. 40, Last sequence up
16-0CT-2001 (Rel. 40, Last senocation)
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                                                                                                                                                                                                                                                                                                                                              QVHWSPGQARLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTTG--STQSNFNF
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             Metazoa;
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                          (Human)
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           Chordata;
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N-LINKED (GLO
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F5/8 TYPE
F5/8 TYPE
MAM.
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CYTOPLASMIC (POTENTIAL).
           Craniata;
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NEUROPILIN-2.
EXTRACELLULAR (POTENTIAL).
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         Vertebrata;
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) (POTENTIAL)
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           Euteleostomi;
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                                                                 factor
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         DOMAIN
TRANSMEM
DOMAIN
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                                                                                       Alternative
SIGNAL
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                                                                                                                                                                                                                                                                                                                           EMBL; AF022859; AAC51788.1; -.
EMBL; AF022860; AAC51789.1; -.
EMBL; AF016098; AAC12922.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the Suropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                              CHAIN
                                                                                                                                PROSITE;
                                                                                                                                               PROSITE;
                                                                                                                                                            PROSITE; PS01285;
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                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                      InterPro; IPR000421;
                                                                                                                                                                                                                                                                                                                  MIM; 602070;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20309748; Put
Gluzman-Poltorak Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-9818099; PubMed-9529250;
Soker S. Takashina S. Miao H -O. Neufeld G. Klagsbrun
"Neuropilin-1 is expressed by endothelial and tumor cells
"secom specific receptor for vascular endothelial growth
cell 92:735-745(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen
                                                                                                                     fransmembrane;
                                                                                                                                                                                                                                                                                                   InterPro; IPR000859;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97470888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neuron 19:547-559(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   affinity receptor for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Neuropilin-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENCE FROM N.A. (ISOFORMS AO AND AL).
INC-97470888; PubMed-9331348:
INC-97470888; PubMed-9331348:
IH, Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne
IH, Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne
IH, Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne
INC-111n-2, a novel member of the neuropilin family, is a land to the company of the neuropilin family.
                                                                                                                                                                                       SM00231; FA58C;
SM00137; MAM; 1.
                                                                                                                                  PS50060; MAM_2;
, Glycop, ve splicing, 20 21 931 21 931 25 889 31 142 267
                                                                                                                                                                                                                                                                         IPR000998; MAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                   squires a license agreement (See http://www.isb-sib.ch/announce/
email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N.A.
                                                                                                                                  FA58C_1;
FA58C_2;
MAM 2; 1
                                                                                                                                                                           CUB;
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                                                                                                                                                                                                                                                                                      CUB.
FA58_C.
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       NEUROPILIN-2.
EXTRACELIULAR (POTENTIAL).
POTENTIAL.
CYTOPIASMIC (POTENTIAL).
CUB 1.
CUB 2.
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                                                                                                                 Neurone; Signal;
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                                                                                         22 (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                               Usage
                                                                                                                   Repeat;
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                                                                                                                                                                                                                                                  RESULT 3
NRP2_MOUSE
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Best Local 9
Matches 109
                                                                                                                   NRP2_MOUSE SYANDAD; PRT; 931 AA.
035375; 035378; 035378; 035378; 035378; 035378;
16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 40, Last snotation update)
Neuropilin-2 precursor (Vascular endothelial cell growth receptor 2).
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CARBOHYD
CARBOHYD
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CONFLICT
SEQUENCE
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DOMAIN
DOMAIN
                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                   NCBI_TaxID-10090;
                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                         420
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                                                                                                                                                                                                                                                                                                                      LRLELFGCRVT 430
                                                                                                                                                                                                                                                                                                                                                       LKVELIGCQIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          POOSRLHGDDNGWTPNLDSN----KEYLQVDLRFLTMLTATATQGAISRETQNGYYVKSY
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FROM N.A.,
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                                                   Chordata; Rodentia;
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ALTERNATIVE SPLICING
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BY SIMILARITY
BY SIM
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Pred. No. 1.1e-18;
                                                 Craniata; Vertebrata;
Sciurognathi; Muridae
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                                                      Muridae;
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                                                                    Euteleostomi;
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SMART; SMO0042; CUB; 2.
SMART; SMO0131; PASSC; 2.
SMART; SMO0137; MAM; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; PASSC_1; 2
PROSITE; PS01285; PASSC_2; 2.
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InterPro; IPR000859; CUB.
InterPro; IPR000421; FA58_C
InterPro; IPR000998; MAM.
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MEDLINE-97470888; PubMed-9331348;
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L; AF022854; AAC53377.1;
L; AF022854; AAC53378.1;
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L; AF022859; AAC53380.1;
L; AF022859; AAC53381.1;
AF022851; AAC5388.1;
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SIMILARITY: CONTAINS 2 CUB DOMAINS.
SIMILARITY: CONTAINS 2 P5/8 TYPE C DOMAINS.
SIMILARITY: CONTAINS 1 MAM DOMAIN.
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AND VEST-145 ISOFORMS OF VEST, AND THE PLGF-2 ISOFORM OF EGF.
SUBUNIT: NUMCOPILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH
RUMCOPILIN-1 IN ONDER TO BE A FUNCTIONAL SEMAPHORIN E RECEPTOR.
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS: 6 ISOFORMS; A22 (SHOWN HERE), A0, A5, A17,
B0 AND B5; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EXPRESSED IN DEFELOPING CNS., PNS AND IN SOME
NONREURAL TISSUES INCLUDING LIMB BUDS. DYPELOPING BONES, MUSCLES,
INTESTINAL EPITHELIUM, KIDNEY, LUNG AND SUBMANDIBULAR GLAND.
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PF00754; F5_F8_type_C;
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GTLPPGTEPTVDTVPVQPIPAYWYYVMAAGGAVLVLASVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVLALVLHYHRERYAAKKTÖHSITYKTSHYINGAPLAVEPT
LITIKLEGERGSHC (IN ISOFORM BO),
VOLPETHGGEGYEDDEIDDEFEGDWSASSSSTSGAGDPSSGK
EKSMLYTLDPILITIIAMSSLGVLLGATCAGLLLLYCTCSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSGKEKSWLYTLDPILITIIAMSSLGVLLGATCAGLLLYCT CSYSGLSSRSCTTLENYNFELYDGLKHKVKINHQKCCSEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALVLHYHRFRYAAKKTDHSITYKTSHYTNGAPLAVEPTLTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           v
                                                                     Craniata; Vertebrata; Euteleostomi
                                                                                                                                                                                                                                                       PRT;
                                                Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTLPPGTEPTVDTVPVQPIPAYWYYVMAAGGAVLVLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76F2443F411D2F63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               343.5; DB
No. 3e-18;
                                                                                                                                                         update)
on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSHC (IN ISOFORM B5)
(IN REF. 1; AAC5338)
                                                                                                                                                                                                                                                          914
                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -KEYLOVDLRFLTMLTAIATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; AAC53380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220
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DISULFID
DISULFID
DISULFID
SEQUENCE
                                            DISULFID
                                                                  DOMAIN
DISULFID
                                                                                      DOMAIN
DOMAIN
                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                   CHAIN
                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                               SMART; SM00042; CUB; 2.
SMART; SM00231; FA58C;
SMART; SM00137; MAM; 1.
                                                                                                                                                                                                                                                                                                                 Pfam; PF00431; CUB; 2.
Pfam; PF00754; F5_F8_type_C;
                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through the swiss institute of Bioinformatics and the 2th the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content use by non-profit institutions as long as its content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Expression of a cell adhesion molecule, developing chick nervous system.";
                                                                                                              DOMAIN
                                                                                                                       DOMAIN
                                                                                                                                  DOMAIN
                                                                                                                                           TRANSMEM
                                                                                                                                                     DOMAIN
                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                  Transmembrane;
                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                              PRINTS; PR00020; MAMDOMAIN
                                                                                                                                                                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                                                                                                                         EMBL; D45416; BAA08256.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fujisawa H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takagi S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-WHITE LEGHORN; TISSUE-Embryonic MEDLINE-95324761; PubMed-7601310;
                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELUILAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY. DEVELOPING NERVOUS SYSTEM: OPTIC TECTI
(LAYERS D AND E OF SGFS), AMACRINE CELLS OF RETINA, NEBERI-
DORSAL ROOT GANGLIA, ALSO EXPRESSED IN MONNEURONAL CELLS,
BLOOD VESSELS IN THE ENTIRE BEBROG
SIMILARITY: DELONGS TO THE MEMBROGIIN FAMILY.
SIMILARITY: COMTAINS 1 CUB DOMAINS.
SIMILARITY: COMTAINS 2 FS/8 TYPE C DOMAINS.
SIMILARITY: COMTAINS 2 TS/8 TYPE C DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE CABDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE PORMATION OF CRETAIN RELEGIANCE, IN ANGIOGENESIS, OUTSIDE THE NER SYSTEM, IT MEDIATRES THE WEEK CHMOREDULANT ACTIVITY OF SEMAPHORIUS SIMILARITY). SEEMS TO HAVE CALCIUM-INDEPENDENT CELL ADHESION REMAINS TO HAVE CALCIUM-INDEPENDENT CELL ADHESION
                                                                                                                                                                                       adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROPERTIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol.
                                                                                                                                                                                                                                                                                                           PF00629; MAM;
                                                                                                                                                                                                          PS01180;
PS01285;
PS01286;
PS00740;
PS50060;
                                                                                                                                                                                                                                                                                                                                                  IPR000859; CUB.
IPR000421; FA58_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170:207-222(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kasuya Y.,
 914
                       848
871
25
145
273
429
636
636
145
273
 8
                                                                                                                                                                                                  Glycoprotein;
                                                                                                                                                                                                          ; CUB; 2.
; FA58C_1;
; FA58C_2;
; MAM_1; 1.
; MAM_2; 1.
                      18
914
847
870
914
139
263
263
422
581
801
102
171
171
  102480
                                                                                                                                                                                                                                                                                                                                          MAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shimizu M.,
                                                                                                                                                                                                                                                                           <u>ب</u>
                                                                                                                                                                                                                                NN
  Ě
           PROBABLE.
PROBABLE.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                           CYTOPLASMIC
CUB 1
CUB 2
                                                                  MAM.
PROBABLE.
                                                                                                 F5/8
                                                                                                                                           EXTRACELLULAR POTENTIAL.
                                                                                                                                                                                                  Neurone;
                                                       PROBABLE
                                                                                                                                                                   NEUROPILIN-1.
                                                                                        8
  DD2EE6D6F0CBB68C
                                                                                      TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matsuura
                                                                                                                                                                                                  Signal;
                                                                                        ဂ ဂ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neuropilin,
                                                                                        2 -
                                                                                                                                  (POTENTIAL)
                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                          http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Η.,
                                                                                                                                                                                                                                                                                                                                                                                                                     Usage
                                                                                                                                                                                                  Repeat; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tsuboi M., Kawakami
  CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I OF THE
IB FORMATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                        no restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                     and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AB)
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Query Match
Best Local Similarity
Matches 115; Conser

Conservative

67;

11.1%; 25.7%;

Score 338; DB Pred. No. 7.6e 67; Mismatches

DB 1;

Length 914;

Indels

86;

Gaps

17;

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RESULT NAME ON NAME OF STREET OF STREET
                                                                                                                                                                                                                                                                                                                                                                                                                       1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                      NRP1_HUMAN
O14786; O60461;
30-MAY-2000 (Re
                                              Gagnon M.L., Bielenberg D.R.,
Soker S., Klagsbrun M.;
                                                                TISSUE-Prostatic adenocarcinoma;
MEDLINE-20183929; PubMed-10688880;
                                                                                                           "Neuropilin-1 is expressed by endothelial and tumor cells isoform-specific receptor for vascular endothelial growth Cell 92:735-745(1998).
                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Neuropilin-1 precursor (Vascular endothelial
                      endothelial growth factor:
                                                                                                                                                  Soker
                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (MEMBRANE-BOUN MEDLINE=97433084; PubMed=9288753; He Z., Tessier-Lavigne M.;
                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                  "Identification of a natural soluble neuropilin-1 that
                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                           MEDLINE=98188099; PubMed=9529250;
                                                                                                                                                                         TISSUE-Breast
                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                     Cell 90:739-751(1997).
                                                                                                                                                                                                                           "Neuropilin is a receptor for the axonal chemorepellent semaphorin
                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                 NRP1 OR NRP OR VEGF165R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   398 LTRFVRIKPVSWENGVSLRFEVYGCKIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QGAISKETKKEYYLKTYRVDVSSNGEDWITLK--EGNKPVVFQGNSNPTDVVYRPFPKPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TG--STQSNENFYVKSFVMNFKNNNSKWKTYKGIVNNEEKVFQGNSNFRDPVQNNFIPPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARYVRVVPQTWHQRIALKVELIGCQIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GILSMVFYTDSAIAKEGFSANYSVSQSSVSEDFQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGQISVLQRKGISRYEGILANGVLSRDGSLSDKRFLFTSNGCSRSLSFEP-----DGQIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILEFESFELEPDSNTPGGAFCRYDRLEI ----WDGFPDVGPHIGRYC-GQNNPGRVRSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DYETHGAGESIRYEVEKRGPECSRNFTSSSGMIKSPGFPEKYPNSLECTYIIFAPKMSEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSHISGRGFLLTY -------ASS------DHPDLITC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LILRIG-DIDIESQTCASDYLLFTSSSDQ----YGPYCGSMTVPKELLLNTSEVTVRFES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LERASHYLKTEYSKFCPAGCRDVAGDISGNMVDGYRDT----SLLCKAAIHAGIIADEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMINFNPHFDLEDRDCKYDYVEVIDGDNAEGRLWGKYCGKI-APPPLVSSGPYLFIKFVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTFTLSRALR----
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                                                                                                                                               Takashima S., Miao H.-Q.,
   Acad
                                                                                                                                                                                                                                                                                                                     (Human)
                                                                                                                                                                                N.A. (MEMBRANE-BOUND
                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
 Sci.
                                                                                       (SOLUBLE/SNRP1 ISOFORM),
                                                                                                                                                                                                                                                             (MEMBRANE - BOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WSSERSRLNY PENGWTPGEDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDKCGDTIKILSPGYLTSPGYPQSYHPSQKCEWLIQAPEPYQR
 U.S
                        H
97:2573-2578(2000).
                        VÍVO
                                                         Gechtman
                                                                                                                                                                                                                                                                                              Craniata; V
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        462
                      expression and
                                                                                                                                                                               ISOFORM),
                                                                                                                                                                                                                                                            ISOFORM)
                                                                                                                                   Neufeld G., Klagsbrun
helial and tumor cells
                                                                                                                                                                                                                                                                                                                                                                                                             923
                                                       Z.,
                                                                                                                                                                                                                                                                                                        Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                             A
                                                                                                                                                                                                                                                                                              Hominidae;
                                                      Miao H.-Q.,
                                                                                         AND SEQUENCE
                                                                                                                                                                               AND SEQUENCE
                                                                                                                                                                                                                                                                                                                                                      cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -VREWIQVDLGLLRFVSGIGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -CMEPLGMESGEIHSDQITV
                      antitumor
                                                                                                                                                                                                                                                                                                                                                   growth factor 165
                                                                                                                                                                                                                                                                                                        Euteleostomi,
                                                                                                                                                                                                                                                                                              Homo
                                  binds vascular
                                                         Takashima
                                                                                         엵
                                                                                                                       M.;
as an
factor.";
                                                                                                                                                                               OF.
                                                                                         22-31
                                                                                                                                                                               22-39
                                                      S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126
 PROSITE;
                                                                                                         PRINTS; PR00020; MAMDOMAIN.
SMART; SM00042; CUB; 2.
SMART; SM00231; FA58C; 2.
SMART; SM00137; MAM; 1.
          CHAIN
                     Alternative
SIGNAL
                                                                                                                                                          Ptam;
                                                                                                                                                                 Pfam; PF00431;
Pfam; PF00754;
                                                       PROSITE;
                                                                           PROSITE;
                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                     MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -
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CHARACTERIZATION.
                                          Fransmembrane; Glycoprotein;
                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                     602069;
                                                                                                                                                        PF00629; MAM;
                                                      PS50060;
                                                                                                  PS01180; CUB;
                                                                PS00740;
                                                                           PS01286;
                                                                                                                                                                                                                       IPR000859; CUB
                                                                                                                                                                                                             IPR000421; FA58_C
                                                                                                                                                                F5_F8_type_C;
                                                                                                                                                                               CUB;
                                                    MAM_2;
                                                               MAM_1;
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8 멅 9 멅 2 맖 Š 밁 5 닭 5 멅 8 멅 9

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Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;
"Neuropilin 2 and neuropilin 1 are receptors for the 165-amino acid
form of vascular endothelial growth factor (VECF) and of placenta
growth factor 72, but only neuropilin 2 functions as a receptor for
the 145-amino acid form of VECF.";
i- FUNCTION: THE MEMBRANE-BOUND ISOFORM IS A RECEPTOR INVOLVED IN vi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20309748; PubMed=10748121;
SOLUBLE/SNRP1 ISOFORMS DOES NOT SEEM TO OVERLAP. THE MEMBRANE-
BOUND ISOFORM IS EXPRESSED BY THE BLOOD VESSUS OF DIFFERENT
TISSUES. IN THE DEVELOPING EMBRYO IT IS FOUND PEDDMINNNTLY IN THE
MERWOUS SYSTEM. IN ADULT TISSUES, IT IS HIGHLY EXPRESSED IN HEART
AND PLACEMEN, MODERAFELY IN LUNG, LIVER, KELEFTAL MISCLE, KIDNEY
AND PLACEMEN, MODERAFELY IN LUNG, LIVER, KELEFTAL MISCLE, KIDNEY
AND PRACERSAS; AND LOW IN ADULT BRAIN. THE SOLUBLE/SNRP1 ISOFORM IS
FOUND IN LIVER HEPATOCYTES, KIDNEY DISTAL AND PROXINAL TUBULES.
SIMILARITY: BELONGS TO THE NUTWOPILLN FRAILY.
SIMILARITY: CONTAINS 2 CUB DOMAINS.
SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
SIMILARITY: CONTAINS 2 THAN DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVELOPMENT OF THE CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN , FORMATION OF CERTAIN REURONAL CIRCUITS AND IN ORGANGENESIS OUTSIDE THE NEWFOUND SYSTEM, IT MEDIATES THE CHEMOREMENIS OUTSIDE THE NEWFOUND SYSTEM, IT MEDIATES THE CHEMOREPOUSANT ACTIVITY OF SEMAPHORINS. IT BINDS TO SEMAPHORIN 3A, THE PIGF-2 ISOSPON OF PGF, THE VEGF-165 ISOSPON OF VGF AND VEGF-B, COEXPERSION WITH KOR RESULTS IN INCREASED VEGF-165 BINDING TO AS WELL AS INCREASED CHEMOTAXIS. IT MAY REGULATE VEGF-INDUCED ANGIOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISOFORM IS SECRETED.
ISOFORM S: MEMBRANE-BOUND (SHOWN
ALTERNATIVE PRODUCTS: 2 ISOFORMS; MEMBRANE-BOUND (SHOWN
ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: THE SCUBLE/SNRP1 ISOFORM BINDS VEST-165 AND APPEARS
TO INHIBIT ITS SINDING TO CELLS, IT MAY ALSO INDUCE APOPTOSIS; I
SEQUESTREING VEGF-165. MAY SIND AS WELL VARIOUS MEMBERS OF THE
SEMMPRORIN FAMILY. ITS EXPRESSION HAS AN AVERSE EFFECT ON BLOOVESSEL NUMBER AND INTERERITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND SOLUBLE/SNRP1; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: THE EXPRESSION OF MEMBRANE-BOUND AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE SOLUBLE/SNRP1
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EMBL; AF018956; AAC51759.1; -. EMBL; AF016050; AAC12921.1; -. EMBL; AF145712; AAF44344.1; -.
            DOMAIN
..06.
..1e; Glyc
./e splicing.
1 21
1 923
3 856
                                                                                                                                                                                                                                                                      IPR001092; HLH_dim IPR000998; MAM.
                                                                                                                ; CUB; 2.
; FA58C_1; 2.
; FA58C_2; 2.
                                                                   Neurone; Signal; Repeat; Receptor;
        EXTRACELLULAR (POTENTIAL)
                        NEUROPILIN-1
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RESULT
NRP1_RAT
ID NRP1
AC Q9QV
DT 16-C
DT 16-C
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Best Local 9
Matches 124
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TRP1_RAT STANDARD; PRT; 090WJ9; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence
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                                                                             o
                                                                                                                             MVSGLISDSQITSSNQGD 454
                                                                                                                                                       LVWRKTSQSTSVSTKKED 485
                                                                                                                                                                                      KPVLFQGNTNPTDVVVAVFPKPLITRFVRIKPATWETGISMRFEVYGCKITDYPCSGMLG
                                                                                                                                                                                                                                                                    NHKPREWLEIDLGEKKKITGIRTIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITVPKG-KRLILRLG-DLDIESQTCASDYL-LFTSSSDQ---YGPYCGSMTVPKELLLN 171
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                                                                                                                                                                                                                   EEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGCQIT----QGNDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                             -CMEALGMESGEIHSDQITASSQYST-----NWSAERSRLNYPENGWTPGEDSY
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N-TINKED (GLONAC...) (POTENTIAL)
N-SEP -> GIK (IN SOLUBLE/SURPI ISOFORM).
X -> E (IN REP. 1)
D -> H (IN REP. 2)
E -> D (IN REP. 2)
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CUB 1.
CUB 2.
F5/8 TYPE C 1.
F5/8 TYPE C 2.
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Pred. No. 1.3e
76; Mismatches
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DISULFID
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1- SIBCELLULAR LOCATION: TYPE I membrane protecin.

1- TISSUE SPECIFICITY: FOUND IN THE EMBRYONIC MERYOUS SYSTEM.

1- SIMILARITY: CONTAINS TO THE MEDIAPOLINE FAMILY.

1- SIMILARITY: CONTAINS 2 CUB DOMAINS.

1- SIMILARITY: CONTAINS 2 FOR TYPE C DOMAINS.
                                                                                                                                       DOMAIN
DOMAIN
                                                                                                                                                                                    DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                          DOMAIN
                                                                             DISULFID
                                                                                                            DOMAIN
                                                                                                                        DOMAIN
                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                       SMART; SM00042; CUB; 2.
SMART; SM00231; FA58C; 2.
SMART; SM00137; MAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00431; CUB; 2.
Pfam; PF00754; F5_F8_type_C;
Pfam; PF00629; MAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF016296; AAC53337.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Neuropilin is a semaphorin III receptor.";
Cell 90:753-762(1997).
-!- FUNCTION: RECEPTOR INVOLVED IN THE DEVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ginty D.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kolodkin A.L., Levengood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40,
Neuropilin-1 precurso
                                                                                                                                                                                                                                                 Transmembrane;
                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97433085;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                            PS01285;
PS01286;
                                                                                                                                                                                                                                                                PS50060;
                                                                                                                                                                                                                                                                                                                           PS01180;
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IPR001092; HLH_dim
IPR000998; MAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR000859; CUB
    645
27
82
147
206
275
431
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                                                                                                                                                                                                                                                                                                                                                                                       MAMDOMAIN
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                                                                                                                                                                                                                                                                                            FA58C_1;
FA58C_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed-9288754;
                                                                                                                                                                                                                                                                                                                           CUB;
    922
855
880
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141
265
424
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583
511
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228
811
173
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  PROBABLE.
PROBABLE.
PROBABLE.
BY SIMILAL
BY SIMILAL
                                                                           MAM.
PROBABLE
                                                                                                                                       CYTOPLASMIC (POTENTIAL)
CUB 1.
CUB 2.
                                                                                                          F5/8
F5/8
                                                                                                                                                                                    EXTRACELLULAR POTENTIAL.
                                                                                                                                                                                                                   POTENTIAL.
NEUROPILIN-1.
                                                                                                                                                                                                                                                 Neurone;
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Sciurognathi; Muridae
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    SIMILARITY
SIMILARITY
                                                                                                          TYPE
                                                                                                                                                                                                                                               Signal;
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                                                                                                                                                                                                                                               Repeat;
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; Murinae; Rat
                                                                                                                                                                                                                                                 Receptor
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RINS. IT
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10 PPM: Thrombin activates factor v proteolytically to the active offector. factor ve (formation of a heavy chain at the meteory chain at the meteory chain at the creaminus).

11 PPM: SULFATION IS REPOLITED TO REFICIENT THROMBIN CLEAVAGE AND ACTIVATION AND POR FULL PROCOMOLIANT ACTIVITY (BY SIMILARITY).

12 PLASTOCYANIN-LIKE REPEATS.

2 PLASTOCYANIN-LIKE REPEATS.

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SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS. SIMILARITY: STRONG, TO COAGULATION FACTOR VIII.

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FAS-BOAR RESULT STATE OF THE ST
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Best Local Si
Matches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FA5_BOVIN S
Q28107; Q28108;
Q1-NOV-1997 (Rel
Q1-NOV-1997 (Rel
16-OCT-2001 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _BOVIN
                                                     MEDILHE-921/538, PubMed-1737753;
Guinto E R.; Esmon C.T., Mann K.G., Macgillivray R.T.;
"The complete cDMA sequence of bovine coagulation factor v.";
. BIOI. Chem. 267:2971-2978 (1992).
'1- PUNCTION: COAGULATION FACTOR V IS A COENCTOR THAT PARTICIPATES
HITH FACTOR XA TO ACTIVATE PROTHROMBIN TO THROMBIN.
'1- SUBUNIT: Pactor Val & composed of a heavy chain and a light chain, noncovalently bound. The interaction between the two child composed control of the chain.
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coagulation
F5.
                                                                                                                                                                                                                                                                                                                                          Bovidae; Bovinae;
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
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SEQUENCE
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics institute. Phere are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P28824;
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                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopodinae;
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                                                 PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITGIRTTGSTQSNFNFYVKSFVMNFKNNNSKWKTYKGIVNNEEKVFQGNSNFRDPVQNNF
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Pinm: pP000754: PS_P8_type_C: 2
Pinm: pP000759: MAN_II.
PINMIS: PR00020: MAMOMAIN.
SMART; SM00042: CUB_2: SMART; SM00042: CUB_2: SMART; SM00040: MAM_II.
PROSITE: PR000040: MAM_II.
PROSITE: PS01180: N58C_II.
                        Transmembrane;
Antigen.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-013758; PubMed-1908252;
Takagi S., Hirata T., Agata K., Mochil M., Eguchi G., Fujisawa H.;
Takagi S., Hirata T., Agata K., Mochil M., Eguchi G., Fujisawa H.;
Takagi S., Hirata T., Agata K., Mochil M., Eguchi G., Fujisawa H.;
Takagi S., Hirata T., Agata K., Mochil M., Eucopalition factors.*;
has homologies to complement components and coagulation factors.*;
Neuron 7:265-207(1991).
Neuron 7:265-207(1991).
PUNCTION. RECEPTOR INVOLVED IN THE DEVELOPMENT OF PROPERTY OF CERTAIN MEMONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NEWFOOLS CERTAIN MEMONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NEWFOOLS SYSTEM. IT MEDIATES THE CHEMORPOUSAND THE NEURONAL AEDCONITION BETWEEN THE OFFIC NERVE FIBERS AND THE VISUAL CENTERS.

1- SUBCELLULAR LOCATION: Type I membrane protein.

1- TISSUE SPECIFICITY: RETINAL GANGLION CELLS AND VISUAL CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuropilin-l recursor (A5 protein) (A5 antigen). Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2180 NPPIISRFIRIIPKTWNQSIALRLELFGCDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Buoinformatics and through EMBL outstation the European Bioinformatics institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00431; CUB; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000859; CUB.
InterPro; IPR000421; FA58_C
InterPro; IPR000998; MAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D10467; BAA01260.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEURONS.

SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY
SIMILARITY: CONTAINS 2 CUB DOMAINS.
SIMILARITY: CONTAINS 2 TE 57/8 TYPE C DOMAINS.
SIMILARITY: CONTAINS 1 MAM DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPPIVARYVRVVPQTWHQRIALKVELIGCQI
                                                                                                                  PS01286; FA58C_2;
PS50060; MAM_2; 1
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                                                                                     Glycoprotein;
21
928
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                                                                                             Neurone; Signal; Repeat; Receptor;
NEUROPILIN-1
                            POTENTIAL.
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RESULT 9

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AC P97333
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DT 16-CCT
DE Neurop
GN NRPI 0
OS MUS mU
OC Eukary
OC Mammal
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Best Local Similarity
Matches 112; Conser
                                       NRPL_MOUSE STANDARD,
p97333;
01-NOV-1997 (Rel. 35, Lc.
01-NOV-1997 (Rel. 35, Lc.
16-CCT-2001 (Rel. 40, Lc.
Neuropiin-1 precursor (
NRP1 OR NRP
          Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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                                  Mus musculus (Mouse)
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                                                                                                                                 SNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGCQIT 462
                                                                                                                                                 QVDLENLRFVSGIGTQGAISKETKKKYFVKSYKVDISSNGEDWITLKD--GNKHLVFTGN
                                                                                                                                                               EIDLGEKKKITGIRTTG--STQSNFNFYVKSFVMNFKNNNSKWKTYKGIVNNEEKVFQGN
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                                                                                                                                                                             LGMESGEIHFDQISVSSQY-----SMNWSAERSRLNYVENGWTPGEDT----VKEWI
                                                                                                                                                                                           LSFEPD----GOIRASSSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSNNHKPREWL
                                                                                                                                                                                                          IGRYCGQNTPGRVRSFTGILSMIFHTDSAIAKEGFFANFSVVQSNTDEDF----
                                                                                                                                                                                                                          LGGQISVLQRKGISRYEGILA----NGVLSRDG-----
                                                                                                                                                                                                                                       EIVLEFESFELEADSN--APGGQTCRYDWLG----IWDGFPG-------VGPH
                                                                                                                                                                                                                                                                                 ESGSHISGRGFLLTY------ASSD------HPDLITC-----
                                                                                                                                                                                                                                                                                                QRIMINFNPHFDLEDRECKYDYVEVIDGDNANGQLLGKYCGKI-APSPLVSTGPSIFIRF
                                                                                                                                                                                                                                                                                                                                           LLALLLAVSAPLRLQAEELGDGCGHLVTYQDSGTMTSKNYPGTYPNHTVCEKTITVPKG-
                                                                                                                                                                                                                                                                                                                             LLSCCCWLLCSLRSSWASRNDKCGDTIKITSPSYLTSAGYPHSYPPSQRCEWLIQAPEHY
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                                            . 35, Created)
. 35, Last sequence upo
.. 40, Last annotation upo
cursor (A5 protein).
                  Chordata;
Rodentia;
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BY SIMILARITY.
N-LINKED (GLCN.
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N-LINKED (GLCN.
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Pred. No. 3.2e-17;
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                Craniata; Veri
Sciurognathi;
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POTENTIAL,
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-LINKED (GLCNAC. .
AF6B323B0A4C789D
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                         Vertebrata;
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                 Muridae;
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                                                                                                                                                                                                                                                                                                                                                                        Length 928;
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               Euteleostomi;
• Murinae; Mus
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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CARBOHYD
SEQUENCE
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CARBOHYD
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DISULFID
                                                                                                           CARBOHYD
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CARBIOVASCILVAE SYSTEM, IN ANGIOGENESIS. IN THE BREMATION OF
CRETAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS
SYSTEM. IT MEDIATES THE CHEMOREULSANT ACTIVITY OF SEMARHORINS. IT
BINDS TO SEMARHORIN 3A, THE PLAP 2 ISONORM OF PGEP, THE VEGET-165
ISOPORM OF VERF AND VEGET-B. COEMPRESSION WITH KOR RESULTS IN
INVERNABLED VEGET-15 BINDING TO KER AS WELL AS INCREASED CHEMOTAXIS.
IT MAY REGULATE VEGET-INDUCED ANGIOGENESIS (BY SIMILARITY).
-: SUBCELLUIAR LOCATION: Type I membrane protein.
-: SIMILARITY: SELONGS TO THE NEUROPILIN FAMILY.
-: SIMILARITY: CONTAINS 2 CUB DOMAINS.
-: SIMILARITY: CONTAINS 2 CUB DOMAINS.
-: SIMILARITY: CONTAINS 2 CUB DOMAINS.
                                                                                                                                                                        DISCLEID
                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
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InterPro; IPR000421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:106206; Nrp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Neurobiol. 29:1-17(1996).
-!- FUNCTION: RECEPTOR INVOLVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuropilin, in the mouse nervous system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kawakami A., Kitsukawa T., Takagi S., Fujisawa "Developmentally regulated expression of a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Embryonic brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96353149; PubMed=8748368;
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PF00754; F5_F8_type_C;
PF00629; MAM; 1.
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SM00137; MAM; 1.
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PS01285; FA58C_1;
PS01286; FA58C_2;
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PS50060; MAM_2;
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103020
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BY SIMILARITY

BY SIMILARITY

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N-LINKED (GLCNAC.

N-LINKED (GLCNAC.

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N-LINKED (GLCNAC.
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CUB 2.
F5/8 T
F5/8 T
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POTENTIAL.
NEUROPILIN-1.
                                                                                                                                                                                                                                        PROBABLE
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CRC64;
           (POTENTIAL).
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MEDILINE-87260865; PubMed-3110773;
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Jenny R.J., Pattman D.D., Toole J.J., Kriz R.W., A
Jenny R.J., Pattman D.D., Toole J.J., Kriz R.W., A
Jenny R.J., Kaufman R.J., Mann K.G.;
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MEDLINE-92222668; PubMed=1567832;
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Cripe L.D., Moore K.D., Kane W.H.
Structure of the gene for human
Sinchemistry 31:3777-3785(1992).
SEQUENCE OF 1188-1215 AND 1315-2224 MEDLINE-86313665; PubMed-3092220; Kane W.H., Davie E.W.;
                                                                                                                                                                                                         MEDLINE-88107560; PubMed-2827731; Kane W.H., Ichinose A., Hagen F.S
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"Crystal structures of the coagulation factor V."; Nature 402:434-439(1999).
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Bertina R.M., Koeleman B.P.C., Koster T., Rosendaal F.F.
Dirven R.J., de Ronde H., van der Valden P.A., Reitsma
Mutation in blood coagulation factor V associated with
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SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
SIMILARITY: STRONG, TO COAGULATION FACTOR VIII.
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DOMAIN: DOMAIN B CONTAINS 35 X 9 AA TANDEM REPEATS,
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s.-T., Pyati J.,
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EMBL: 132766 AAB59001
EMBL: 132767 AAB59001
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InterPro: IPR000421; Rx58_C.
Pfam; PP00734; Cu-oxidase; 3.
Pfam; PP00734; FS_F8_type_C; 2.
SYART; SW00231; FX58C; 2.
PROSITE; PS00079; MULTICOPPER_OXIDASE1; 2.
RXSSITE; PS01245; FA58C_1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blood coagulation; Glycoprotein; Sulfation; Calcium; Signal; Zymogen;
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.. REPEATS.

4 AA REPEATS IN BOVINE FAS.
45 X 9 AA APPROXIMATE TANDEM REPEATS OF
[TMP]-L-S-P-D-L-S-Q-T.
1102 2-2
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F5/8 TYPE A 1.
PLASTOCYANIN-LIKE
PLASTOCYANIN-LIKE
F5/8 TYPE A 2.
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ACTIVATION PEPTIDE (CONNECTING REGION)
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                   Score 317; Ub .,
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                              Length 2224;
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                     16;
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FA5_PIG Q9GLP1; 16-OCT-2001 16-OCT-2001 01-MAR-2002 Coagulation FA5_PIG (Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
factor V precursor (Activated protein (Rel. STANDARD; Created 2258 ₽

Eukaryota; Sus scrofa (Pig)

cofactor).

NCBI_TaxID=9823; Mammalia; Eutheria; Metazoa; Cetartiodactyla; Chordata; Craniata; Vertebrata; Euteleostomi; actyla; Suina; Suidae; Sus.

MEDLINE=21121490; PubMed=11229814; Grimm D.R., Colter M.B., Braunschw Kim H.K.W.; TISSUE-Liver; DOMAINS SEQUENCE FROM N.A., AND 3D-STRUCTURE MODELING OF F5/8 TYPE × AND 0

Braunschweig M., Alexander L.J., Neame

P.J.,

Cell. Nol. Life Sci. 58:148-159(2001).

- FUNCTION: Coagulation factor V is cofactor that participates
- in the factor X at oractivate prothrombin to thrombin.
- i- SUBUNIT: Factor Va is composed of a heavy chain and a light protein modeling of domains."; "Porcine factor V: cDNA cloning, gene mapping, three-dimensional protein modeling of membrane binding sites and comparative anato

anatomy

of

is calcium-dependent. chain, noncovalently bound. The interaction between the two

chains

DOMAIN: Domain B contains 41 x 9 AA tandem repeats. Domains C1 and C2 may be involved in membrane binding. PTM: Thrombin activates factor V protectlystically to the active coffector. factor Va (formation of a heavy chain at the N-terminus and a light chain at the C-terminus). STATIANTY: CONTAINS 3 F5/8 TYPE A DOMAINS; EACH IS COMPOSED 01 2 PLASTOCYANIN-LIKE REPEATS. ç

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the EMPL outstation in the EMPL property of the EMPL outstation to the EMPL outstation on the EMPL outstation of the EMPL outstation of the Swiss by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch)
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Blood coagulation; Glycoprotein; Sulfation; Calcium;
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InterPro; IPR001117; Cu-oxidase.
InterPro; IPR000421; FA58 C.
Pfam; PF00394; Cu-oxidase; 3.
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LIGHT CHAIN (BY SIMILARITY).
P5/8 TYPE A 1.
PLASTOCYANIN-LIKE 1.
PLASTOCYANIN-LIKE 2.
P5/8 TYPE A 2.
PLASTOCYANIN-LIKE 3.
PLASTOCYANIN-LIKE 4.
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41 X 9 AA APPROXIMATE TANDEM
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COAGULATION FACTOR V.

HEAVY CHAIN (BY SIMILARITY).

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PLASTOCYANIN-LIKE
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F5/8 TYPE C 2.
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Lactadherin (formerly BA46), a membrane-associated glycoprotein
expressed in human milk and brast carcinomas, promotes Arg-Gly-Asp
(RGD) dependent cell adhesion.";
DNA Cell Biol. 16:861-869(1997).
1 FUNCTION: MAY BE INVOLYED IN PHOSPHOLIPID BINDING BINDS
SPECIFICALLY TO ROTAVIRUS AND INHIBITS ITS REPLICATION.
1 FUNCTION: MEDIN IS THE MAIN CONSTITUENT OF MORTIC MEDIAL AMYLOID
1 SUBCELLUAR LOCATION: PERIPHERAL MEMBRANE PROTEIN.
1 TURSUB SPECIFICITY: MAMARY BETTHERIA DESIGNES
1 TURSUB SPECIFICITY: MAMARY BETTHERIA TOTAL
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KEDLINE-97405885; PubMed-9260929;

MEDLINE-97405885; PubMed-9260929;

"" w R., Couto J.R., Scallan "" na46), a m
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Proc. Natl. Acad. Sci. U.S.A. 96:8669-8674(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BA6 reveals an RCD cell adhesion sequence presented on an epidermal DNA Cell Biol. 15:281-286(1996).
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MEDLINE-91371351; PubMed-1909932
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Ceriani R.L.;
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01-NOV-1997 (Rel. 35,
16-OCT-2001 (Rel. 40,
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Mammalia; Eutheria;
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16-007-2001 (Rel. 40, Last annotation update)
Lactadherin precursor (Hilk fat globule-Egef factor 8) (MFG-E8) (HMFG)
(Breast epithelial antigen BA46) (MFGM) (Contains: Medin].
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FYM: MEDIN HAS A RAGGED N-TERMINUS WITH MINOR 
AMINO ACID 264 AND 273. 
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN. 
SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
        SWISS-PROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             breast tumors contains factor VIII-like domains."; es. 51:4994-4998(1991).
                                                                                                     SPECIFICITY: MAMMARY EPITHELIAL CELL SURFACES AND AORTIC
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Catarrhini; Hominidae
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human milk fat globule membranes.";
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P7049;
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Ol-NOV-1997 (Rel. 35, Created)
Ol-NOV-1997 (Rel. 35, Last sequence update)
Ol-NOV-1997 (Rel. 39, Last annotation update)
Ol-MAY-2000 (Rel. 39, Last annotation update)
Lactadherin precursor (Milk fat globule-Egg factor
           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
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               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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Ggura K., Mara K., Watanabe Y., Kohno K., Tai T.,

"Cloning and expression of cDNA for O-acetylation
ganglioside.";
ganglioside.";
Biochem. Biophys. Res. Commun. 225:932-938(1996).
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Pfam; PF00754; P5_F8_type_C;
PRINTS; PR00010; EGFELOOD.
SMART; SM00181; EGF; 2.
SMART; SM00231; FA58C; 2.
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SEQUENCE
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SIGNAL 1 2
CHAIN 23 42
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PROSITE: PS01186: EGF 2; 2.
PROSITE: PS01285: FA58C_1; 2.
PROSITE: PS01286: FA58C_2; 2.
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SEQUENCE FROM N.A
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DENCTION: AMY BE INVOLVED IN HORSEFHOLIDID BINDING. SEEMS TO PARTICIPATE IN THE O-ACCEYLATION OF GD. CANGLIOSIDE SIALICA SUBCELLULAN LOCATION. PERIPHERN. MEMBANE PROTEIN

11SSUE SPECIFICITY: SPLEEN, LUNG, HEART, BRAIN AND MUSCLE, SIMILARITY: COMPAINS 2 EGG-LIKE DOMAINS.

SIMILARITY: COMPAINS 2 F5/8 TYPE C DOMAINS.
                                                                                                      TEYTCQCPVGYSGIHCELGCSTKLGLEGGAIAD----
ARLYRTGIVNAWTASSYDSKPWIQVDFLRKMRVSGVMTQGA-SRAGRAEYLKTFKVAYSL
                                                         SVLQRKGI----
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                                                                                                                                                                                                                                                                       Similarity
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IPR001438; EGF_II.
IPR000421; FA58_C.
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EGE-LIKE 1.

EGE-LIKE 2.

P5/8 TYPE C 1.

P5/8 TYPE C 2.

EY SIMILARITY.

BY SIMI
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Pred. No. 3.1e-15;
4; Mismatches 96;
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MEDLINE-86081164; PubMed-3935400;
Truett M.A., Blacher R., Burke R.L., Caput D., Chu C., Dina D.,
Truett M.A., Blacher R., Burke R.L., Caput D., Chu C., Dina D.,
Hartog K., Kuo C.H., Masiarz F.R., Merryweather J.P., Najarian R.,
Pachl C., Potter S.J., Puma J., Ouiroga M., Rall L.B., Randolph A.,
Urdea M.S., Valenzuela P., Dahl H.-H.M., Favalaro J., Hansen J.,
Urdea M.S., Valenzuela P., Dahl H.-H.M., Favalaro J., Hansen J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Cr
21-JUL-1986 (Rel. 01, La
01-MAR-2002 (Rel. 41, La
Coasgulation factor VIII
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                                                                                                                                                                                                                                                                                                                                                                                                  MEDIJINE-85061550; PubMed-6438528; Toole J.J., Knopf J.L., Wozney J.M., Pittman D.D., Kaufman R.J., Brown E., Amphlett G.W., Foster W.B., Coe M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wood W.I., Capon D.J., Simonsen C.C., Eaton D.L., Gitschier J.,
Keyt B., Seeburg P.H., Smith D.H., Hollingshead P., Wion K.L.,
Delwart E., Tuddenham E.G.D., Vehar G.A., Lavn R.M.,
"Expression of active human factor VIII from recombinant DNA clones.";
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                                                                                                                                                                                                                             Gitschier
                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                         Amphlett G.W., Foster W.B
Hewick R.M.;
"Molecular cloning of a c
Nature 312:342-347(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 312:330-337(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-85061548; 1
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      SULFATION
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MEDLINE-88191889;
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ntonarakis S.E.,
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RESULT 15

WFOLMOUSE

AC 21355, P97800;

DT 01-AUG-1991 (Rel. 10, Last sequence update)

DT 01-AUG-1991 (Rel. 40, Last sequence update)

DT 16-CCT-2001 (Rel. 40, Last sequence update)

DE Lactadherin precursor (Milk fat globule-EEF fact)

EXECT-2001 (Rel. 40, Last sequence)

CR MFGEB.

OS Mus masculus (Mouse).

OK MFGEB.

OS Mus masculus (Mouse).

OK MFGEB.

OK 
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                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restructed by one profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend.onemail to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Mammary gland;
MEDLINE-1046608; PubMed-2122462;
Stubbs J.D., Lekutis C., Singer K.L., Bui A., Yuzuki Srinivasan U., Parry G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *cDNA cloning of a mouse mammary epithelial cell surface protein reveals the existence of epidermal growth factor-like domains linked to factor VIII-like sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE PROTEIN.
-1- TISSUE SPECIFICITY: MAMMARY EPITHELIAL CELL SURFACES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 NGCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSNNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE FROM NONPREGNANT ANIMALS & MAXIMAL I SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS. SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
FUNCTION: MAY BE INVOLVED IN PHOSPHOLIPID BINDING. ZONA PELLUCIDA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEVELOPMENTAL STAGE: MRNA EXPRESSION IS DETECTABLE IN MAMMARY TISSUE FROM NONPREGNANT ANIMALS & MAXIMAL IN THE LACTATING GLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KPREWLEIDLGEKKKITGIRTTGSTQSNFNFYVKSFVMNFKNNNSKWKTYKGIVNNEEKV 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NSCSMPLGMESKAISDAQITASSYFTNMFAT----WSPSKARLHLQGRSNAWRPQVNN-
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Pred. No. 2.9e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87:8417-8421(1990)
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                                                                                                                                                                                                                                                                                                                  http://www.isb-sib.ch/announce/
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Best Local Similarity
Matches 112; Conser
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SIGNAL
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PROSITE: PS01186; EGF_2; 2.
PROSITE: PS01285; FA58C_1;
PROSITE: PS01286; FA58C_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00008; EGF; 2.
Pfam; PF00754; F5_F8_type_C;
PFINTS; PR00010; EGFBLOOD.
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SMART; SM00231; FA58C; 2.
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  352
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KINAW----TAQSNSAKEWLQVDLGTQRQVTGIITQGARDFGHIQYVESYKVAHSDDGVQ
                                 P--SWASGDSSNNHKPREWLEIDLGEKKKITGIRTTGSTQSNFNFYVKSFVMNFKNNNSK 401
                                                                                                                                                                                                               GLQRWGPELARLYRTGIVNAWHASNYDSKPWIQVNLLRKMRVSGVMTQGA-SRAGRAEYL
                                                                                                                                                                                                                                                                                  NLDGEYMFTTAVPNTAVPTPAPTPDLSNNLASRCSTQLGMEGGAIADSQISASYVYMGFM 174
                                                                                                                                                                                                                                                                                                                                                                                           LLTYAS-----SDHPDLITCLERASHYLKTEYSKFCPAGCRDVAGDISGNM-
                                                                                                                                                                                                                                                                                                                                                                                                                               CASG--LFAASGD----FCDS-----SLCLN------GGTCLTGQDNDIYCLCPEGF
                                                                     CTLRFELLGCELHGCLEPLGLKNNTIPDSQMSASSSYKTWNLRA--FGWYPHLGRLDNQG
                                                                                                         -SLSFE----
                                                                                                                                          KTFKVAYSLDGRKFEFIQDESGGDKEFLGNLDNNSLKVNMFNPTLEAQYIRLYPVSCHRG
                                                                                                                                                                              ----SLSDKRFLFTSN-----
                                                                                                                                                                                                                                                   ---ELGGQISVLQRKGI
                                                                                                                                                                                                                                                                                                                         -VDG-YRDTSLLCKAAI-----
                                                                                                                                                                                                                                                                                                                                                          TGLVCNETERGPCSPNPCYNDAKCLVT-LDTQRGDIFTEYICQCPVGYSGIHCETETNYY
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EGG-LIKE 1.
EGG-LIKE 2.
EGGLARATIY.
EY SIMILARITY.
EY SIMILARIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59;
                                                                                                      ----PDGQIRASSSWQSVNESGDQVHWSPGQARLQDQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 276.5; DB 1;
Pred. No. 1.4e-13;
9; Mismatches 118;
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                                                                                                                                                                                                                                                                                                                         EGF-like domain;
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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        Score
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Gapop 10.0 , Gapext 0.5
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3052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      July 9, 2002, 02:14:03 ; Search time 130,73 Seconds (without alignments) 773.433 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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096907 homo sapien
091262 homo sapien
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096288 rattus nory
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ALIGNMENTS

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DR CRE	RA RA	R R R R R	RRRR	RRR	RA R R R R	200055	RESULT Q9D4J3 ID Q AC Q DT 0
Punctional annotation of a full-length mouse cDNA collection.; Nature 409.685-690(2001)	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch KF., Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.,	Blake J., Bottelli D., Bojunga N., Carninci P., de Bonado M.F., Brownstein M.J., Bult C., Pletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Riowald M., Rodrinez T. Sakamoro N. Nordone P., Ring B., Riowald M., Rodrinez T.	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schrinl L.M., Staubii F., Suzuki R., Tomita M., Nagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,	Yamanaka Wa T., Saito Casavant T.	Ishii	4631413K11RTK, PROTEIN. 4631413K11RTK, PROTEIN. 4631413K11RTK, PROTEIN. Mis musculus (Mouse). Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bummalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NPBT TexTP-10000.	1 9D4J3 PRELIMINARY; PR 9D4J3, PRELIMINARY; PR 1-JUN-2001 (TrEMBLES 17, Creat 1-JUN-2001 (TrEMBLES 17, Last 1-DAY-2001 (TREMBLES 17, Last 1-DAY-2001 (TREMBLES 17, Last

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4631413K11RIK PROTEIN.
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InterPro; IPRO04043; LCCL.
Pfam; PF00431; CUB; 1.
SMART; SM00042; CUB; 1.
SPOUENCE 503 AA: 54547 MW;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
                                                         SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-SKIN,
MEDLINE-21085660; PubMed-11217851;
                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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Rodentia;
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Sciurognathi; Muridae; Murinae; Mus
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No. 2.5e-96;
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InterPro: IPRO00859; CUB.
InterPro: IPRO04043; LCCL.
Pfam: PF00431; CUB: 1.
SMARR: SM0042; CUB: 1.
PROSITE: PS00140; CUB: 1.
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Local Similarity 48.8%;
hes 237; Conservative 2
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                                        PRELIMINARY
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Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schrimi L.M., Staubii F., Suzuki R., Tomita M., Wagyner L., Washio T., Sakai K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo N.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Kombaerts P., Kordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Kordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Haveshzeh Y., Kohtsuki S.,
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Nature 409:655-690(2001)
-1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
EMBL; AK014521; BAB29409 1;
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Pred. No. 6.6e-84;
4; Mismatches 26
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     Q91ZV3
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Matsumori A., Sasayama S., Honjo T., Tasahiro K.;
"ESDN. a Novel Neuropilin'like Nembrane Protein Cloned
Cells with the Longest Secretory Signal Sequence among
Up-regulated after Vascular injury",
U Blook Chem. 276.34105-3414(2001).
EMBL: AF987549, AAL30180.1;
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
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                                                                                                                                              EMTQKLDLITSDMA
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  PRELIMINARY
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  PRT;
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No. 1.4e-66;
769
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Matsumori A., Sasayama S., Honjo T., Tashiro K.,
ESDN, a kovel Neuropilin-like Membrane Protein Cloned
cells with the Longest Secretory Signal Sequence among
Up-regulated after Vascular Injury.",
J. Biol. Chem. 276:34105-34114(2001).
EMBL. AF387548, ALAJO179.1;
SEQUENCE 769 AA: 83774 MW; 73CIF1646FA3F017 CRC64;
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Mammalia; Eutheria;
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                                                    KEMTOKLDLITSDMA
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                                                                                                                                -----RKKKKKGSPYGSAEAQKTDCWKQIKYPF--
                                                                                                                                                                                                                                                       NPVQWQQKIAMKVELLGCQFTLKGRLPKLTPPPRNGNN---LRNTTARPKLGKGRAPKFT
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(TremBirel. 19, Last sequence update)
(TremBirel. 19, Last sequence update)
AND SMOOTH MUSCLE CELL-DERIVED NEUROPILIN-LIKE
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Rodentia;
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Sciurognathi; Muridae; Murinae; Mus
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Eukaryotes, Is
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Kobuke K., Furukawa Y., Sugai M., Tanigaki K., Ohashi N. Matsumori A., Sasayama S., Honjo T., Tashiro K.; ESDN, a Novel Neuropilin-like Membrane Protein Cloned Cells with the Longest Secretory Signal Sequence among Up-regulated after Vascular Injury.", J. Biol. Chem. 276:34105-34114(2001).
EMBL. AF385273, BALOJIR B.; SEQUENCE 775 AA: 85034 MW; 3D06F81EF2337010 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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SYDNEKEMTOKLDLITSDMA
                                                    VCAWHWRNRKKKTEGTYDLPYW---
                                                                                                                                                                                                                                                                                                                                                                   EHNYYVSAYRILYSDDGQKWTVYREPGVEQDKIFQGNKDYHQDVRNNFLPPIIARFIRVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYQDSGTMTSKNYPGTYPNHTVCEKTITVPKGKRLILRLGDLDIE-SQTCASDYLLFTS-
                                                                                                                                                     FTQPLQPRSSNEFPAQTEQTTASPDIRNTTVTPNVTKDVALAAVLVPVLVMVLTTLILIL
                                                                                                                                                                                                          ITRPI------PSEET--STGINITT
                                                                                                                                                                                                                                                              PTQWQQKIAMKMELLGCQFIPKGRPPKLTQPPPPRNSND----LKNTTAPPKIAKGRAPK
                                                                                                                                                                                                                                                                                                                  PQTWHQRIALKVELIGCQ - - - - - - - ITQ - - - - - GNDSLVWRKTSQSTSVSTKKEDET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VNESGDOVHWSPGQARLODOGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTTGSTQS
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(TYEMBLIE1. 19, Last sequence update)
(TYEMBLIE1. 19, Last sequence update)
AND SMOOTH MUSCLE CELL-DERIVED NEUROPILIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                     RKKKKKGS---PYGSAEAOKTDCWKOIKYPF--
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; Pred. No. 1.6e
106; Mismatches
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                                                    -DRAGWWKGMKQFLPAKAVDHEETPVRYSSSE--V
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Best Local
Q9H2E2;
Q9H2E2;
01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00431; CUB; 1.
Pfam; PF00754; F5_F8_type_C;
SMART; SM00042; CUB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D29810; BAA18909.1; -.
InterPro; IPRO00859; CUB.
InterPro; IPRO00421; FA58_C.
InterPro; IPRO04043; LCCL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "unpublished.";
Submitted (APR-1994)
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                     GNKRIITRMVRNNFLPPIIAR
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                                                                                                                                                                                                                                                                                          QIDLNKEKKITGIITTGSTMVSTITMCLPTESCTVMMGRNG----
                                                                                                                                                                                                                                                                                                                                           EIDLGEKKKITGIRTTGSTQ-SNFNFYVKS---FVMNFKNNNSKWKTYKGIVNNEEKVFQ 417
                                                                                                                                                                                                                                                                                                                                                                                               SGGD-RGSSNNSITVLEW--TDHTGQENSWKPKKSQAE---KTWTALGAFATDE--YQWL
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(TremBLrel. 01, Last sequence update)
(TremBLrel. 19, Last annotation update)
   (TrEMBLrel. 16,
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                                                       PRELIMINARY;
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AINS 1 CUB DOMAIN.
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Pred. No. 1.0
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Best Local
 Q9H2E4;
01-MAR-2001
01-MAR-2001
                              Q9H2E4
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Pfam; PRO0431; CUB; 2.
SMART; SMO0231; FASBC; 1.
SMART; SMO0231; FASBC; 1.
PROSITE: PS01180; CUB; 2.
PROSITE: PS01285; FASBC; 1; UNKNOWN_1.
SEQUENCE 555 AA; 62430 MW; B67B7C99ZAB0546F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isoforms.";
Genomics 70:211-222(2000).
Genomics 70:211-222(2000).
-i- SIMILARITY: CONTAINS 2
EMBL; AF280546; AAG41405.1;
HSSP; P12259; 1CZT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rossignol M., Gagnon M.L., Klagsbrun M. and Neuropilin-2 
"Genomic Organization of Human Neuropilin-1 and Neuropilin-2 
Identification and Distribution of Splice Variants and Solub
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01-DEC-2001 (
NEUROPILIN-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-PROSTATIC ADENOCARCINOMA;
MEDLINE-20564205; PubMed-11112349;
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Mammalia; Eutheria;
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Homo Sapiens (Human).
Chordata;
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                                                                             LRLELFGCRVT 430
                                                                                                              KLEVSTNGEDWMVYRHGKNH--KVFQANNDATEVVLNKLHAPLLTRFVRIRPQTWHSGIA
                                                                                              LKVELIGCQIT 462
                                                                                                                                 VMNFKNNNSKWKTYKGIVNNEEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIA 451
                                                                                                                                                   PQQSRLHGDDNGWTPNLDSN----KEYLQVDLRFLTMLTAIATQGAISRETQNGYYVKSY
                                                                                                                                                                       PGQARLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTTG--STQSNFNFYVKSF
                                                                                                                                                                                          FSARYYLVHQEPLENFQ-----CNVPLGMESGRIANEQISASSTY-----SDGRWT
                                                                                                                                                                                                            ILANGVLSRDGSLSDKRFLFTSNGCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWS
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                                                                                                                                                                                                                                                  -CPAGCRDVAGDIS--GNMVDGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRYEG
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                                                                                                                                                                                                                                                                                                                                                                    CGHLVTYQDSGTMTSKNYPGTYPNHTVCEKTITVPK-GKRLILRLG-DLDIESQTCASDY 145
                                                                                                                                                                                                                                                                                                                               LLF----TSSSDQYGPYCGSMTVPKELLLNTSEVTVRFESGSHISGRGFLLTY-----AS
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(TrEMBLrel. (TrEMBLrel.
                              PRELIMINARY;
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Last sequence update)
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Pred. No. 2.
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Catarrhini; Hominidae; Homo.
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Query Match
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SMART: SMOD42 CUB: CUB: SMART: SMOD31: PR580: 2.
SMART: SMOD31: PR580: 2.
SMART: SMOD317: MAM: 1.
PROSITE: PS01120: CUB: 2.
PROSITE: PS01205: FA580: 1: U
PROSITE: PS01205: FA580: 1: U
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-: SIMILARITY: CONTAINS 2 CUB D
-: SIMILARITY: BELONGS TO THE I
-: SIMILARITY: CONTAINS 1 MAM D
ENEL AF280544; AAG41403.1; --
HSSP; P12259; 1CZT
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Mossignol M., Gagnon M.L., Klagsbrum M.;
Genomic Organization of Human Neuropiin-1 and Neuropi
Identification and Distribution of Splice Variants and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000421; FA58_C.
InterPro; IPR000998; MAM.
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LRLELFGCRVT 430
                                    LKVELIGCQIT
                                                                                                                                                                             PGQARLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTTG--STQSNFNFYVKSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGHLVTYQDSGTMTSKNYPGTYPNHTVCEKTITVPK-GKRLILRLG-DLDIESQTCASDY
                                                                   KLEVSTNGEDWMVYRHGKNH--KVFQANNDATEVVLNKLHAPLLTRFVRIRPQTWHSGIA
                                                                                                       YMNFKNNNSKWKTYKGIVNNEEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIA
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                                                                                                                                              -KEYLQVDLRFLTMLTAIATQGAISRETQNGYYVKSY
                                                                                                                                                                                                                         -CNVPLGMESGRIANEQISASSTY -----
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Pred. No. 4.8e-19
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NEUROPILIN FAMILY.
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1F3107A9CC665EA2
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Prim: PPO0432; MAM; 1.
PRINTS: PRO0422; MAM; 1.
PRINTS: PRO0424; CUB; 2.
SMART: SM00424; CUB; 2.
SMART: SM00137; MAM; 1.
PROSITE: PS01180; CUB; 2.
PROSITE: PS01285; FX58C_1; UNKNOWN_1.
PROSITE: PS01285; FX58C_1; UNKNOWN_1.
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Q9H2D5;
01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomics 70:211-222(2000).
-!- SUBCELLULAR LOCATION: TYPE
-!- SIMILARITY: CONTAINS 2 CUB
-!- SIMILARITY: BELONGS TO THE
-!- SIMILARITY: CONTAINS 1 MAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-2056/205; PubMed-11112349;
MEDLINE-2056/205; PubMed-11112349;
Ressignol M. Gegnon M.L. Klagsbrun M.;
"Genomic Organization of Human Neuropilin-1 and Neuropilin-2
Identification and Distribution of Splice Variants and Solubl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein; Neurone; Receptor; Transmembrane SEQUENCE 901 AA; 101381 MW; Al310304AFD0867
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InterPro; IPR000998; MAM.
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HSSP; P12259; 1CZT.
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                                                                                                                                           DCKYDWLDIWDGIPHVGPLIGKYCGTKTPSELRSSTGILSLTFHTDMAVAK------DG
                                                                                                                                                                                                    EDCSKNFTSPNGTIESPGFPEKYPHNLDCTFTILAKPKMEIILQFLIFDLEHDPLQVGEG
                                                                                                                                                                                                                                                                                                                  CGGRLNSKDAGYITSPGYPQDYPSHQNCEWIVYAPEPNQKIVLNFNPHFEIEKHDCKYDF
VMNFKNNNSKWKTYKGIVNNEEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIA
                          PQQSRLHGDDNGWTPNLDSN----KEYLQVDLRFLTMLTAIATQGAISRETQNGYYVKSY
                                                      PGQARLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTTG--STQSNFNFYVKSF
                                                                                     FSARYYLVHQEPLENFQ-----CNVPLGMESGRIANEQISASSTY-----SDGRWT
                                                                                                               ILANGYLSRDGSLSDKRFLFTSNGCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWS
                                                                                                                                                                        -CPAGCRDVAGDIS--GNMVDGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRYEG
                                                                                                                                                                                                                                                           IEIRDGDSESADLLGKHCGNI-APPTIISSGSMLYIKFTSDYARQGAGFSLRYEIFKTGS
                                                                                                                                                                                                                                                                                                                                                                        109;
                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                     72;
                                                                                                                                                                                                                              -HPDLITC----LERASHYLKTEYSKF----
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                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 4.8e-19;
                                                                                                                                                                                                                                                                                                                                                                                                   Score 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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DOMAINS.
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 901;
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RESOLUTION OF THE PROPERTY OF 
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Q9H2E3;
Q1-MAR-2001
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01-MAR-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
NEUROPILIN-2B(5).
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-i SIMILARITY: CONTAINS 2 CUB
-i SIMILARITY: BELONGS TO THE
-i SIMILARITY: CONTAINS 1 NAM
EMBL: AF280545; AAG41404.1; -.
HSSP; P12259; 1CZT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein; Neurone; Receptor; Transmembrane SEQUENCE 906 AA; 101955 MW; 0FB01F24D8D9B01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE: PS01180; CUB; 2.
PROSITE: PS01285; FA58C_1; UNKNOWN_1
PROSITE: PS50060; MAM_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00042; CUB; 2.
SMART; SM00231; FA58C; 2.
SMART; SM00137; MAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00431; CUB; Pfam; PF00629; MAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000859; CUB.
InterPro; IPR000421; FA58_C
InterPro; IPR000998; MAM.
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KEDLINE-20546205; PubMed-11112349;

KESIJUNE-20546205; PubMed-11112349;

Geonomic Organization of Human Neuropilin-1 and Neuropilin-2 Genes:
Identification and Distribution of Splice Variants and Soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0020; MAMDOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomics 70:211-222(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-9606;
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ILANGYLSRDGSLSDKRFLFTSNGCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWS
                                                                                                                                                                                                                                                                                                                                                                                                                                             CGHLVTYQDSGTMTSKNYPGTYPNHTVCEKTTTVPK-GKRLILRLG-DLDIESQTCASDY 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLEVSTNGEDWMYYRHGKNH--KVFQANNDATEVVLNKLHAPLLTRFVRIRPQTWHSGIA 419
                                                                        DCKYDWLDIWDGIPHVGPLIGKYCGTKTPSELRSSTGILSLTFHTDMAVAK----
                                                                                                                                                                                EDCSKNFTSPNGTIESPGFPEKYPHNLDCTFTILAKPKMEIILQFLIFDLEHDPLQVGEG
                                                                                                                                                                                                                                                                                        IEIRDGDSESADLLGKHCGNI-APPTIISSGSMLYIKFTSDYARQGAGFSLRYEIFKTGS 146
                                                                                                                                                                                                                                                                                                                                     LLF----TSSSDQYGPYCGSMTVPKELLLNTSEVTVRFESGSHISGRGFLLTY----AS 196
                                                                                                                                                                                                                                                                                                                                                                                             CGGRLNSKDAGYITSPGYPQDYPSHQNCEWIVYAPEPNQKIVLNFNPHFEIEKHDCKYDF
                                                                                                                         -CPAGCRDVAGDIS--GNMVDGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRYEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.4%;
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                                                                                                                                                                                                                                    -HPDLITC----LERASHYLKTEYSKF-----
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Last annotation update)
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Pred. No. 4.9e-19
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IE NEUROPILIN FAMILY.
M DOMAIN.
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334 PGARRICOGESPANSOSSNINERPENDIAGENCE PARSON PETVKSF 305 PQGSRIHGDDMGWTPHLDSN	₽ 29	оy	Db Qy	Man Que			488888	RRRRRR	2 2 2 2 2 2 S		RESULT Q9H2D4 ID Q	B Q	р	Db Qy	Дb
	.97 SD	LLPTSSSDQYGPYCGSMTVPKELLLNTSEVTVRFESGSHISGRGFLLTYAS : : : : : :	CGHLVIYQDSGTWTSKNYPGTYPNHTVCEKTITVPK-GKRLIIRLG-DLDIESQTCASDY	tch 11.4%; Score 349; DB 4; Length 906; cal Similarity 25.3%; Pred. No. 4.9e-19; 109; Conservative 72; Mismatches 166; Indels 84; Gaps 1	UNKNOWN_1. ptor; Transmembrane. MW; EB183F265457B0B9	InterPro; IPR000859; CUB, InterPro; IPR000421; PA58_C. InterPro; IPR000999; MAM. Pfam; PF00431; CUB; 2. Pfam; PF00431; CUB; 2. Pfam; PF00431; CUB; 2. Pfam; PF00431; CUB; 2.	EMBRANE PROTEIN (BY SIMILARITY) MAINS RODPILIN FAMILY. MAIN.	un M.; uropilin-1 and Neuropilin-2 Splice Variants and Solubi	niata; Vertebrata; Euteleos arrhini; Hominidae; Homo.	(TrembLrel. 16, Created) (TrembLrel. 16, Last sequence up (TrembLrel. 19, Last annotation B(5).	11 9H2D4 PRELIMINARY; PRT; 906	52 LKVELIGCQIT :: :: 20 LRLELFGCRVT	WHERKMASKHETYKGIVNEEKYEGONSHEDEVONETEPTVARVENVEGTHIGGEA KLEVSTNGEDMYVTHIGKHHKVEQANNDATEVVLNKLHAPLLTREVETERQTHISGIA	PGQARLQDQGFSWASGDSSNNHKPREWLEIDLGEKKKITGIRTTGSTQSNFNFYVKSF 	260 FSARYYLVHQEPLENFQCNVPLGMESGRIANEQISASSTYSDGRWT 305

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Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
EMBL, BC007737, AB407377, 1;
SEQUENCE 609 AA; 68347 MW; 798AAFD2D568C127 CRC64;
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Ol-DEC-2001 (TTEMBLEEL 19, Last sequence update)
Ol-DEC-2001 (TTEMBLEEL 19, Last annotation update)
SIMILAR TO NEUROPILIN 1.
Homo sapians (Human)
EURATYOta: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Manmalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID-9606;
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Q96190;
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354 NHKPREWLEIDLGEKKKITGIRTTG--STOSNENEYVKSFVMNEKNNNSKWKTYKGIVNN 411
                                                                                                                                                                                        298
                                                                                                                                                                                                                                                                                                              253 AG-IIADELGGQI------SVLQRKGISRYEGILANGVLSRDGSLSDKRFLF 297
                                                                                                                                                                                                                                                                                                                                                                                                        176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 TSEVTVRFESGSHISGRGFLLTYA------205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 TITVPKG-KRLILRLG-DLDIESQTCASDYL-LFTSSSDQ---YGPYCGSMTVPKELLLN 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420 LRLELFGCRVT 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362 KLEVSTNGEDWMYYRHGKNH--KVFQANNDATEVVLNKLHAPLLTRFVRIRPQTWHSGIA 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 LIQAPDPYQRIMINFNPHFDLEDRDCKYDYVEVFDGENENGHFRGKFCGKI-APPPVVSS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 RGL-----LALLLAVSAPLRLQARELGDGCGHLVTYQDSGTMTSKNYPGTYPNHTVCEK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 FSARYYLVHQEPLENFQ------CNVPLGMESGRIANEQISASSTY------SDGRWT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             278 ILANGVLSRDGSLSDKRFLFTSNGCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWS 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 DCKYDWLDIWDGIPHYGPLIGKYCGTKTPSELRSSTGILSLTFHTDMAVAK------DG 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 RGLPLLCAVLALVLAPAGAFR-----NDKCGDTIKIESPGYLTSPGYPHSYHPSEKCEW 56
                                                                                                   ----CMEALGMESGETHSDOITASSQYST------NWSAERSRLNYPENGWTPGEDSY 322
                                                                                                                                                                     TSNGCSRSLSFEP----DGQIRASSSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSN 353
                                                                                                                                                                                                                                            IGRYCGQKTPGRIRSSSGILSMVFYTDSAIAKEGFSANYSVLQSSV-SEDFK------
                                                                                                                                                                                                                                                                                                                                                                                     IVFAPKMSEIILEFESFDLEPDSNP--PGGMFCRYDRLEI----WDGFPD-----VGPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----LERASHYLKTEYSKFCPAG--CRDVAGDISGNMVDGYRDTSLLCKAAIH 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VMNFKNNNSKWKTYKGIVNNEEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIA 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.0%; Score 335; DB 4; Length 609; 24.9%; Pred. No. 3.5e-18; ative 76; Mismatches 176; Indels 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0961H5; PRELIMINARY; PRT; 0961H5; 01-DEC-2001 (TEEMBLrel. 19, Created) 01-DEC-2001 (TEEMBLrel. 19, Last seq 01-DEC-2001 (TEEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streusberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC007533; AAH07533.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE-KIDNEY, AND RENAL CELL ADENOCARCINOMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEUROPILIN 1.
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                                                                                                                                                                        KPVLFQGNTNPTDVVVAVFPKPLITRFVRIKPATWETGISMRFEVYGCKITDYPCSGMLG
                                                                                                                                                                                                                                                                                     ----REWIQVDLGLLREVTAVGTQGAISKETKKKYYVKTYKIDVSSNGEDWITIK--EGN
                                                                                                                                                                                                                                                                                                                                                                                                      ----CMEALGMESGEIHSDQITASSQYST-----NWSAERSRLNYPENGWTPGEDSY 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSNGCSRSLSFEP----DGQTRASSSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSN 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AG-IIADELGGQI------SVLQRKGISRYEGILANGVLSRDGSLSDKRFLF 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IVFAPKMSEIILEFESFDLEPDSNP--PGGMFCRYDRLEI----WDGFPD-----YGPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----LERASHYLKTEYSKFCPAG--CRDVAGDISGNMVDGYRDTSLLCKAAIH 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPFLFIKFVSDYETHGAGFSIRYEIFKRGPECSQNYTTPSGVIKSPGFPEKYPNSLECTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIQAPDPYQRIMINFNPHFDLEDRDCKYDYVEVFDGENENGHFRGKFCGKI-APPPVVSS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RGLPLLCAVLALVLAPAGAFR------NDKCGDTIKIESPGYLTSPGYPHSYHPSEKCEW 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGL-----LALLLAVSAPLRIQAEELGDGCGHLVTYQDSGTMTSKNYPGTYPNHTVCEK 117
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                                                          MVSGLISDSQITSSNQGD
                                                                                                                                                                                                                              EEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGCQIT----QGNDS
                                                                                                                                                                                                                                                                                                                                                NHKPREWLEIDLGEKKKITGIRTTG--STQSNFNFYVKSFVMNFKNNNSKWKTYKGIVNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGRYCGQKTPGRIRSSSGILSMVFYTDSAIAKEGFSANYSVLQSSV-SEDFK------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7533; AAH07533.1; -.
644 AA; 71907 MW; 9204B6F5C3CD2A21 CRC64;
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Last annotation update)
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Pred. No. 3.8e-18;
6; Mismatches 176; Indels 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo
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InterPro; IPR000421; FAS8_C.
Pfam; PF00431; CUB; 2.
SMART; SM00042; CUB; 2.
SMART; SM000221; FAS8C; 2.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; FAS6C_1: 1.
SEQUENCE 704 AA; 79002 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissup-maosmaric AdemocrationA;
MEDLINE-2054.015, pubmed-lili2349;
MEDLINE-2054.025, pubmed-lili2349;
Genomic Organization of Human Neuropilin-1 and Neuropilin-2 Ge Genomic Organization of Human Neuropilin-1 and Neuropilin-2 Ge Identification and Distribution of Splice Variants and Soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NRP1.
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09H2E1;
01-MAR-2001 (TIEMBLIEL 16,
01-MAR-2001 (TIEMBLIEL 16,
01-DEC-2001 (TIEMBLIEL 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics 70:211-222(2000).
-!- SIMILARITY: CONTAINS 2:
EMBL; AF280547; AAG41406.1;
HSSP; P12259; 1CZT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEUROPILIN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 TITVPKG-KRLILRLG-DLDIESQTCASDYL-LFTSSSDQ---YGPYCGSMTVPKELLLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 RGL------LALLLAVSAPLRLQAEELGDGCGHLVTYQDSGTMTSKNYPGTYPNHTVCEK
LVWRKTSQSTSVSTKKED 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPFLFIKFVSDYETHGAGFSIRYEIFKRGPECSQNYTTPSGVIKSPGFPEKYPNSLECTY
                                                                                     KPVLFQGNTNPTDVVVAVFPKPLITRFVRIKPATWETGISMRFEVYGCKITDYPCSGMLG
                                                                                                                                                                                                                                                                                                                                                                       TSNGCSRSLSFEP----DGQIRASSSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IVFAPKMSEIILEFESFDLEPDSNP--PGGMFCRYDRLEI----WDGFPD-----VGPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSEVTVRFESGSHISGRGFLLTYA------SSDHPDLITC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIQAPDPYORIMINENPHEDLEDRDCKYDYVEVFDGENENGHERGKECGKI-APPPVVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGLPLLCAVLALVLAPAGAFR-----NDKCGDTIKIESPGYLTSPGYPHSYHPSEKCEW
                                                                                                                                            EEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGCQIT----QGNDS
                                                                                                                                                                                                       ----REWIQVDLGLLRFVTAVGTQGAISKETKKKYYVKTYKIDVSSNGEDWITIK--EGN
                                                                                                                                                                                                                                                      NHKPREWLEIDLGEKKKITGIRTTG--STOSNFNFYVKSFVMNFKNNNSKWKTYKGIVNN
                                                                                                                                                                                                                                                                                                                                                                                                                                     IGRYCGQKTPGRIRSSSGILSMVFYTDSAIAKEGFSANYSVLQSSV-SEDFK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------LERASHYLKTEYSKFCPAG--CRDVAGDISGNMVDGYRDTSLLCKAAIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                · IIADELGGQI--------SYLQRKGISRYEGILANGVLSRDGSLSDKRFLF
                                                                                                                                                                                                                                                                                                                        -CMEALGMESGEIHSDQITASSQYST-----NWSAERSRLNYPENGWTPGEDSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 0%; Score 335; DB 4; 24.9%; Pred. No. 4.4e-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS: PRO0020, MANDOMAIN.
SMART: SMO0042; CUB: 2.
SMART: SM00021; PA58C; 2.
SMART: SM00117; MAN; 1.
PROSITE: PS01180; CUB: 2.
PROSITE: PS01280; PA58C; 2.
PROSITE: PS01280; PA58C; 2.
PROSITE: PS01280; MAN; 1.
PROSITE: PS0160; MAN; 2. 1.
PROSITE: PS0160; MAN; 2. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein;
SEQUENCE 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00431; CUB; 2.
Pfam; PF00754; F5_F8_type_C;
Pfam; PF00629; MAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000859; CUB.
InterPro; IPR000421; FA58_C.
InterPro; IPR001092; HLH_dim.
InterPro; IPR000998; MAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=97433084; PubMed=9288753;
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Eŭkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell 90:739-751(1997)
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III.";
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                                                            181 MSEIILEFESFDLEQDSNP--PGGMFCRYDRLEI----WDGFPE
                                                                                                                                                                       121 KFVSDYETHGAGFSIRYEIFKRGPECSQNYTAPTGVIKSPGFPEKYPNSLECTYIIFAPK 180
                                                                                                                                                                                                                                    178
                                                                                                                                                                                                                                                                                                                                          124 G-KRLILRLG-DLDIESQTCASDYLLFTSSSDQ----YGPYCGSMTVPKELLLNTSEVTV 177
                                                                                                                                                                                                                                                                                         62
                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 RGLLALLLAVSAPLRLQAEELGDGCGHLVTYQDSGTMTSKNYPGTYPNHTVCEKTITVPK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
ELGGQISVLQRKGISRYEGILA-----NGVLSRDGSLSDKRFLFTSNG-----CSRSLSFE 309
                                                                                                              ----LERASHYLKTEYSKFCPAG--CRDVAGDISGNMVDGYRDTSLLCKAAIHAGIIAD 258
                                                                                                                                                                                                                            RFESGSHISGRGFLLTYA--------SSDHPDLITC-----
                                                                                                                                                                                                                                                                                     PYQRIMINFNPHFDLEDRDCKYDYVEVIDGENEGGRLWGKFCGKI-APSPVVSSGPFLFI 120
                                                                                                                                                                                                                                                                                                                                                                                                   RGLPLLCATLALALGAFR-SDKCGGTIKIENPGYLTSPGYPHSYHPSEKCEWLIQAPE 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neurone;
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103052 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.7%; Score 325.5; DB 11; Length 921; 24.0%; Pred. No. 3.8e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Transmembrane.
58B29A9AA4978971 CRC64;
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222 HIGRYCGQKTPGRIRSSSGILSMVFYTDSAIAKEGFSANYSVLQSSISEDFKCMEALGME

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388 DVVFGVFPKPLITREVRIKPASWETGISMRFEVYGCKIT 426
                                            424 DPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGCQIT 462
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                                                                                                                               366
                                                                                                                                                                        282
                                                                                                                                                                                                            310 P----DGQIRASSSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSNNHKPREWLEIDL
                                                                                     GLLRFVTAVGTQGAISKETKKKYYVKTYRVDISSNGEDWITLK--EGNKAIIFQGNTNPT 387
                                                                                                                            GEKKKITGIRTTG--STOSNFNFYVKSFYMNFKNNNSKWKTYKGIVNNEEKVFQGNSNFR 423
                                                                                                                                                                     SGEIHSDQITASSQYGT-----NWSVERSRLNYPENGWTPGEDSY----REWIQVDL
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Search completed: July 9, 2002, 02:25:21 Job time: 678 sec

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Result
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                   Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Query
Score Match Length DB
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1761
1 atgggattcggtgcggggca.....caagtgatatggcaggttaa 1761
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Copyright (c) 1993 - 2000 Compugen Ltd.
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253508 Seque	5350	σ	6996		78.4
112722	11272	0	5035		8
0713	7130	σ	5035		8
R034084	3408	9	5035		.80
146888 S	88	0	4999		
R138378 Sequence	13837	0	4999		
008904 High le	BD008904	6	4670	4.5	78.4
110040 Sequenc	04	σ	4670		.00
641 Sequence		σ	4551		80
8643 Sequence		σ	4281		80
644 Sequence 4	44	6	4278		80
22513 Homo sap	BC022513	9	2536		8
707 H	HUMF8C	9			8
5352	AX253521	σ	10698		æ
53510	AX253510	σ	8720		80
2925		10	6585		0
59794 Sequen		Φ	7032		81.6
16234		4	7032		Ë
189 Canis		4	7145		Ü
308 Sus scro	AF191308	4	7062		~
7 Human coa	77	9	6909		2
Me.	75	6	6909		.2
885 Sequenc	AX146885	6	6909		2
379		σ	6909		.~
e S	A63218	σ	6909		92.8
5 Sequence 1	A46255	S	6909		2
5 Huma	HUMFVA	9	6893		4
0 Bos	BOVEACV	4	6910	٠	
1 Bos taurus	N	4	6895	•	95
2052	HSA420528	9	2072		31
9810 Human mRNA	HUMCUB1	9	1388	7.5	132.8
026646 Homo s	02664	2	4	6	34
9	8	N			159
026646 Homo	02664	N	4	2.4	
O'L'A' NACCAS	5 5	, م	0	_	2
F3875/40 Da++16	R75	10	2339	2	20
387547 Homo a	AF387547	9	2939		
56350 Homo can	6350	٥	2020		8
387548 Mine	875	10		ω.	29
132671 Human	DJ920	9		4	
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118816 Seguenc	1881	6	9	ω.	
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ALIGNMENTS

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	11761	source
	Lexicon Genetics Incorporated (US) Location/Qualifiers	FEATURES
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and gene encoding the same		TITLE
	Sands, A.T.	
iedrich, G., Zambrowi	Donoho, G., Turner, C.A., Nehls, M., Friedrich, G., Zambrowicz, B. and	AUTHORS
	1 (bases 1 to 1761)	REFERENCE
hini; Hominidae; Hom	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
ta; Vertebrata; Eute	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	ORGANISM
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	AX118818.1 GI:14035775	VERSION
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Hominidae
1 (Dases I to 1620)
Donobo G. Turner, C.A., Nehls, M., Friedrich, G., Zaml
Sands, A.T.
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Sequence
AX118822
                                                 Human cub-domain-containing protein Patent WO 0129219-A 7 26-APR-2001; Lexicon Genetics Incorporated (US) Location/Qualifiers
                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae 1 (bases 1 to 1768)
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Query Match Best Local Similarity

86.4%; 100.0%;

Score 1522; DB 6; Pred. No. 1.2e-280;

Length 1768;

QY 당 왕

Oy 1080 gctggagatcgatttgggggagaaaagaaataacaggaattaggaccacaggatctac	Oy 720 tagagatacctctttattgtgcaaagctgccatccatgcaggaataattgctgatgaact 779	Matches 1522; Conservative 0; Mismatches 0; Indels 0; Great Conservative 0; Great Great Conservative 0; Great Great Great Conservative 0; Great
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et 1557 T 1260	ggaataaacattacaacggtggctattccattggtgctccttgttgtcctggtgtttgc 	1498 1201	Db Qy
:a 1497 - :A 1200	TCAACTAAGAAAGATGAGACAATCACAAGGCCCATCCCCTCGGAAGAAAACATCCAC	1141	B 8
114	AGATTACACAAGGTAATGATTCATTGGTGTGGCGCAAGACAAGTCAAAGCACCAGTC	80	B B
143	agattacacaaggtaatgattcattggtgtgtggcgcaagacaagtcaaagcaccagtgt	1378	VQ
545	gggttgtcccccaqoatggcacagaggatagccttgaaggtggagctcattggttg	1318 1021	Db Oy
9 13 - 10	CCABACTICOGGACCCAGTGCAAAACAATTTCATCCCTCCCATCGTGGCCAGATATGT	961	B 4
c 125	craagrigaagacctaraaaggaattiggaataatgaagaaaaggigtttcaagggtaa 	0 4	B 5
T 90	ACAGTCGAACTTTATGTTAAGAGTTTTGTGATGAACTTCAAAAACAATAA	841	문
11	cacagtcgaacttcaacttttatgttaagagttttgtgatgaacttcaaaaacaa	1138	Qy
# 1137 - # 840	Tegertegaegarcyartteggegegaaaaagaaaaraacaggaattaggaccacaggatct	1078 781	Db Qy
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72	GGCAGTCGGTCAATGAGAGTGGAGACCAAGTTCACTGGTCTCCTGGCCAAGCCAAGGTCGACGTCTCCTGGCCAAGCCAAGCT	661	ov p
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4	TCTGCCAGCTGGTTGTAGAGACGTAGCAGGAGACATTTCTGGGAATATGGTAGATG	361	B
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laa 657 AA 360	COGGETTHATHACATGTTTGGAACGAGCTAGCCATTATTGAAGACAGAATACAGCAA	301	B 6
∃ –	GTGGATCCCACATTTCTGGCCGGGGTTTTTTGCTGACCTATGCGAGCAGCAGCGACCA	4	рb
59	agagtggatcccacatttctggccggggttttttgctgacctatgcgagcagcgac	1.0	Qy
24	GGAAGTATGACTGTTCCCAAAGAACTCTTGTTGAACACAAGTGAAGTAACCGTCCGCTTT	181	Db
t 53	gaagtatgactgttcccaaagaactcttgttgaacacaagtgaagtaaccgtccgc	478	Qy
3T 180	ACCTGTGCTTCTGACTATCTTCTCTTCACCAGCTCTTCAGATCAATATGGTCCATACTG	121	Db

AUTHORS AUTTUR TITLE JOURNAL	SULT 5 099419/c CUS FINITION CESSION RESION FENITS SYMORDS ORGANISM	Oy 1558 99 Db 1261 66 Oy 1618 90 Db 1321 60 Oy 1678 to Oy 1578 at Db 1381 70 Oy 1738 at
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COMMENT
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TITLE
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Direct Submission

Direct Submission

Submitted (15-NVP2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

This sequence version replaced gi:17149292:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    findPhrapList
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NOTE: This is a "working draft' sequence. It currently consists of 42 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number will be preserved.
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Center clone name: CH230-8N22
Cummary Statistics
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Contact: hgsc-help@bcm.tmc.edu
Project Information
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4: gap of unknown length
1: contig of 18137 bp in length
1: gap of unknown length
0: contig of 16249 bp in length
0: gap of unknown length
2: contig of 9692 bp in length
2: contig of 9692 bp in length
5: contig of 1383 bp in length
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449 gctcttcagatcaatatggtccatactgtggaagtatgactgttcccaaagaactcttgt 508
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mes 500; Conserv
                                                  GGTT--GAGATITGAACACTGATTCCAAGACCTGTGCTTCCGACTATCTCCTCTTCAGCA 4371
                                                                    ggttgggagatttggatatcgaatcccagacctgtgcttctgactatcttctcttcacca 448
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20.4%;

Score 359.6; DB 2; Pred. No. 1.5e-58; 0; Mismatches 129;

Indels 13; Gaps Length 249429;

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BASE COUNT ORIGIN		FEATURES Source																																							
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47319 c 45841 g	<pre>'organism="Rattus nor 'db_xref="taxon:10116 'chromosome="Mcs1" 'clone="CH230-8N22"</pre>	.249429		248361:	248261:	245828:	728.	587:	549:	242449:	239570:	23/766:	: 999	621:	521:	826.	726:	285	426:	326:	888:	788	397:	300	•••	543:	443:	200	831	731:	641:	5	20	יטכ	198401:	194203:	94103:	0282:	90182	562	552
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                        The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: mr. PMBL. SN: SNISSPROT; Tr: TREMEL; Wp: WORMPDP; Information on the WOMMPDP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6. constructed by the Sanger Centre Chromosome 6. constructed by the Sanger Centre Chromosome 6 constructed by the Sanger Centre Chromosome 6 was plant of the Sanger Centre Chromosome 6 was plant of the Sanger Centre Chromosome 6 was plant of the Sanger Control of the Roswell Park in the Chromosome 6 was plant of the Roswell Park provided by the Chromosome 6 was plant of the Roswell Park provided by the Chromosome 6 was plant of the Roswell Park provided with the Chromosome 6 was plant of the Roswell Park provided with the Roswell Park provided was plant of the Roswell Park provided with the Roswell Park provided was plant of the Roswell Park provided wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                requests: clonerequestesanger.ac.uk
On Aug 22, 2000 this sequence version replaced gi:7228316.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                  annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
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Manmalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 131060)
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         Institute by the group of Pieter de Jong. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (21-AUG-2000) Sanger Centre, Hinxton, Cambridgesh.
UK. E-mail enquirles: humquery@sanger.ac.uk Clone
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425. .513
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                                                        .6143 of
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/note="MER41B 15991. .16301

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24622. .25110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"AluJ repeat: matches 144../304 of consensus" 22605. .22747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="LIMC1 repeat: matches 6189. .6327 of consensus" 21601. .21760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MIR repeat: matches 48. 20926. .21059
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19570. .19759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Aluy repeat: matches 1, .311 of consensus" 18848 19305
                                                                                                                                                                                                                                                                                                                                                                       /note="AluJo repeat: matches 3. 33294. .33430
                                                                                                                                                                                                                                                                                                                                                                                                             /note="U6 repeat: matches 1. .10? of consensus" 32842. .32990 / 32842. .32991 / 33915. .33293 of consensus" 33015. .33293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Lopes 29 mer 73% conserved" ...
/Note-"Lopes 29 mer 73% conserved" ...
28958. .29218
/note-"LlME3A repeat: matches 5319. .5594 of consensus"
29994 . .2942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="L1M4 repeat: matches 2707. .2830 of consensus" 26862. .28116
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26590. .26692
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23693..24058
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                                                                                                                      /note="LIMB7 repeat: matches 5694. 39205. .39278
                                                                                                                                                          /note="MER81 repeat: matches 1. 38453. .38920
                                                                                                                                                                                                                                 /note="AluJb repeat: 37633. .37939
                                                                                                                                                                                                                                                                   34753
                                                                                                                                                                                                                                                                                                      /note-Min repeat: matches 67. .142 of consensus 34337. .34618
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                                                    /note="AluJb repeat: matches 3. 41119. .41144
                                                                                        /note="MIR repeat: matches 117.
39919. .40220
                                                                                                                                                                                                /note="AluJb repeat: matches 3.
38218. .38311
                                                                                                                                                                                                                                                                                                                                        /note="AluJ repeat: matches 1 .138 of consensus" 33881 .33949
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/note="AluJo repeat:
                                   /note="13 copies 2 mer ac 100% conserved"
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  matches
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Matches 257; Conserv
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Sasayama, S., Matsumori, A., Honjo, T. and Tashiro, K.
Direct Submission
                                                                                                                                                                                                          I (bases 1 to 26/2)

Kobuke K., Prinkawa Y., Sugai, M., Tanigaki, K., Ohashi, N.,

Kobuke K., Prinkawa Y., Sugai, M., Tanigaki, K., Ohashi, N.,

Matsumori, A., Sassyama S., He heimorane protein Cloned from Vascular

ESIN, a Novel Neuroplihin-like bendbrane protein Cloned from Vascular

Cells with the Longest Secretory Signal Sequence among Eukaryotes,

IS Up-regulated after Vascular Injury

Libol. Chem. 276 (38), 3405-3414 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus strain ICR neuropilin-like protein AF387548
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                                                           University Graduate School of Medicine,
Sakyo-ku, Kyoto 606-8501, Japan
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
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                                                                                                               Submitted (30-MAY-2001) Department of Medical Chemistry, Kyoto
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44928. .45276
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44551, .44785
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42077. .42367
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/db_xref="taxon:10090"
                 /strain-"ICR"
                                  /organism="Mus musculus"
                                                     1. . 2642
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                                                                                                  Yoshida Konoe-cho
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tacagcaaattctgcccagctggttgtagagacgtagcaggagacatttctgggaatatg
                                                                                       agcgaccatccagatttaataacatgtttggaacgagctagccattatttgaagacagaa
                                                                                                                                                   GTGCTGTTCATGAGTGGAACCCCATGCTGCTGGGGGAGGATTTTTGGCTTCATACTCAGTT
                                                                                                                                                                                                                                                 TACTGTGGTCTGGGTTTACAAATGAATCAGTCAATTGAGTCCAAAGGCAGTGAAGTCACA
                                                                                                                                                                                                                                                                                                                                                  CACCTTAATTACCTGAAAATCTTTAATGGAATTGGAGTCAGCAGAACGGAAATAGGCAAA
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                                                  ATAGATAAAGAAGATTTAATCACTTGTTTGGATACTGTATCTAATTTTTTGGAACCAGAG
                                                                                                                                                                                                  gtccgctttgagagtggatcccacatttctggccggggttttttgctgacctatgcgagc
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Biol. Chem. 276 (36),
a 703 c 744 g
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/protein_id="AAL30179.1"
/protein_id="AAL30179.1"
/db_xref="G1:16902437"
/translation="MASRAFLRAARSPOGFGGPAPAATGRAALPSAGCCPLEPGRNS
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RTGERIRIKFGDFDIEDSDYCHLNYLKIFNGIGVSRTEIGKYGGLGLONNGSIESKGS
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KGRLPKLTPPPRNGNNLRNTTARPKLGKGRAPKFTQVLQPRSRNELPVQPAETTTTPD
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ISGTIPHGYRDSSPLCMAGIHAGVVSNVLGGQISIVISKGTPYYESSLANNVTSTVGY
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314. .2623
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HPTASVGLPSTSTFKTAGTQPHALVGTYNTLLSRTDSCSSGQAQYDTPKGGKSAATPE
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/codon_start=1
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gene sequence in GenBank Accession
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Sekine, M., Kikuchi, H.,

Kanda, K.,

Wagatsuma, M.,

Takahashi-Fujii,A.

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RESULT
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Kusano, J., Watanabe, M., Fujimori, K., Tanai, H., Ishida, M., Yamashita, H., Chiba, Y., Sugiyama, T., Irie, R., Otsuki, T., Wakamatsu, A., Ishii, S., Yamamoko, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Matsuo, K., Nakamura, Y.,
                                                                                                 Ishibashi,T., Kanehori,K., Yosida,M., Watanabe,S.,
Ono,Y., Hotuta,T., Hiraoka,S., Murakawa,K., Takiguo
                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                          Homo sapiens
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Direct Submission
Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute.
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Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
NEDO human cDNA sequencing project
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RESULT AF387547 REFERENCE SOURCE LOCUS REFERENCE DEFINITION FEATURES KEYWORDS VERSION ACCESSION TITLE JOURNAI TITLE AUTHORS ORGANISM JOURNAL AUTHORS PUBMED Submitted (30-MAY-2001) Department of Medical Chemistry, Kyoto University Graduate School of Medicine, Yoshida Konoe-cho, Sakyo-ku, Kyoto 606-8501, Japan 2 (bases 1 to 2939) Kobuke, K., Furukawa, Y., Susasayama, S., Matsumori, A., Direct Submission Cells with the Longest Secretory Signal Sequence among Eukaryotes. Is Up-regulated after Vascular Injury J. Biol. Chem. 276 (56), 34105-34114 (2001) Matsumori,A., Sasayama,S., Honjo,T. and Tashiro,K.
ESDN, a Novel Neuropilin-like Membrane Protein Cloned from Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (basea 1 to 2939)

Kobuke,K., Furukawa,Y., Sugai,M., Tanigaki,K., Ohashi,N., Homo sapiens neuropilin-like protein AF387547 AF387547 2939 bp mRNA linear PRI 11-NOV-2001 Homo sapiens endothelial and smooth muscle cell-derived 11447234 Location/Qualifiers Sugai,M., Tanigaki,K., A., Honjo,T. and Tashire (ESDN) mRNA, complete cds Tashiro, K. Ohashi, N., Vascular

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                                                                                              Kobuke,K., Furukawa,Y., Sugai,M., Tanigaki,K., Ohashi,N., Sasayama,S., Matsumori,A., Honjo,T. and Tashiro,K.
                                                                                                                                                                            Marsumort.A. Sasayama.S. Honjo,r. and Tashiro,K.
ESDN. a Novel Neuropilin-like Nembrane Protein Cloned from Vascular
Cells with the Longest Secretory Signal Sequence among Eukaryotes,
IS Up-regulated after Vascular Injury
J. Biol. Chem. 276 (36), 3410-4414 (2001)
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RESTLUS norvegicus endothelial and smooth muscle cell-derived neuropillin-like protein (Esdn) mNNA, complete cds.

AF887549.

GE:16902438
                University Graduate School of Medicine, Sakyo-ku, Kyoto 606-8501, Japan
                                                       Submitted (30-MAY-2001) Department of Medical Chemistry, Kyoto
                                                                                   Direct Submission
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Kobuke, K., Furukawa, Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gatagiggcacaaigacaictaagaaitaiceegggacetaeeeeaateaeacigiitge 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGCTCCCGGACGCTGGAGCCCAGAAAGGTGATGGATGTGGACACACTGTACTAGGCCCT 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ccgctccggctgcaggcggaggagctgggtgatggctgtggacacctagtgacttatcag 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCCTCCCTGGCCGCAACTCCTCCTCCAGGCCTCGGCTGCTCCTTCTACTGCTCCTA 179
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                                                                                                 TCCAAAGGCAGTGAAATCACAGTGCTGTTCATGAGTGGAATCCATGCTTCTGGTCGAGGA
                                                                                                                                               ttgaacacaagtgaagtaaccgtccgctttgagagtggatcccacatttctggccggggt
                                                                                                                                                                                                     AGCAGAACGGAAATAGGCAAGTACTGTGGTCTGGGTTTACAAATGAATCAGTCAATTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="endothelial and
neuropilin-like protein"
/protein_id="AAL30180.1"
/db_xref="GI:16902439"
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KGRLFKLTOPEPERUSNILKNTTVERKJGRAFKETOALOPESINJLFLLFAOTTALE
KGRLFKLTOPEPERUSNILKNTTVERKJGRAFKETOALOPESINJLFLLFAOTTALEHD
KAGMKGVKQLLPAKSVEHEETPVKYSNSEVSHLSPREVTTVLQADSAEYAOPLVGGI
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EITVLFMSGIHASGRGFLASYSVIDKQDLITCLDTVSNFLEPEFSKYCPAGCLLPFAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MASRAPIRAARSPQDPGGRAAPAATGRAPIPSAGWCPIPPGRNS
SSRPRILLLLLLLLPDAGAQKGDGCGHTYLGPESGTLTSINYPHTYPNSTYCKWEIRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="Esdn"
12. .2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSTASVGLPSTSTFRTAGNQPPALVGTYNTLLSRTDSCSSGQAQYDTPKGGKPAAAPE
ELVYQVPQSTQEASGAGRDEKEDAFKETL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VGTLHQRSTFKPEEGKEASYADLDPYNAPVQEVYHAYAEPLPVTGPEYATPIVMDMSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPGAAQDKIFQGNKDYHKDVRNNFLPPIIARFIRVNPVQWQQKIAMKVELLGCQFTI
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PPWAAFATDEHQWLQIDLNKEKKITGIVTTGSTLIEHNYYVSAYRVLYSDDGQKWTVY
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/codon_start-1
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Pred. No. 3.6e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tggcaccagaggatagccttgaaggtggagctcattggttgccagattacac 1387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTCGTAATAACTTTTTGCCACCAATTATTGCACGTTTCATTAGAGTGAACCCTGTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gtgcaaaacaatttcatccctcccatcgtggccagatatgtgcgggttgtcccccagaca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aaaggaattgtgaataatgaagaaaaggtgtttcagggtaactctaactttcggggaccca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAGGTGTGATCGCCGATCCCCAGATAACAGCATCATCTGTACTGGAGTGGACTGACCAC
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                                      Submitted (08-AUG-1997) Chromosome 6 Project Group (http://www.sanger.ac.uk/HGP/Chr6/) Sanger Centre, Cambridgeshire, CB10 ISA, UK. E-mail enquires:
humqueryesanger.ac.uk Clone requests: clonerequestesanger.ac.uk
on Aug 14, 1997 this sequence version replaced gi:1842200.
                                                                                                              Direct
                                                                                                                                Phillips, S.
                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known such as compressions and repeats, but not necessarily within known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 with a note of the overlapping clone name. Note that the variations annotated may not be found in the sequence submission corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMPORFANT: This sequence is the entire insert of clone 9d(16. 
During sequence assembly data is compared from overlapping clones 
Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Institute by the group of Pieter de Jong.
For further details see http://bacpac.med.buffalo.edu/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94G16 is from the library RPCI1 constructed at the Roswell Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The true left end of clone 94G16 is at 1 in this sequence. The true right end of clone 94G16 is at 100808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  feature key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the overlapping clone as we submit sequences with only a small
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                           /note="AluSx repeat: matches 16740. .16877
                                                                                                                                                                                                                                                                                                                                                                                                                                             6052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MER42c repeat: matches 983. .690 of consensus" 5738. .5790
/note="MIR2 repeat: matches 144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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1. .100808
                                                                                      note-"AluY repeat: matches 1.
                                                                                                                                       ncomplete repeat"
                                                                                                                                                          /note-"AluSp repeat:
                                                                                                                                                                                                        /note="L1MD1 repeat: matches
                                                                                                                                                                                                                                 /note="AluJb repeat; matches
12013. .12188
                                                                                                                                                                                                                                                                                                  ncomplete repeat"
                                                                                                                                                                                                                                                                                                                           /note="AluSx repeat:
                                                                                                                                                                                                                                                                                                                                                                   /note="MIR repeat: matches 262. .47 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="MER5A repeat: matches 131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="MER42B repeat: matches 1204.
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/note="15 copies of 2 mer 100 % conserved"
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/clone_lib="RPCI-1"
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                                                                          .14096
                                                                                                                                                                                      .12500
                                                                                                                                                                                                                                                                                   .11890
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                                              .3 of consensus*
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                               50140. .50235
/note--FLAM_A repeat: matches 133. .40 of consensus
51950. .52234
                                                                                                                                                                               /note="2 copies of 49349. .49557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1/538. .17591
/note="2 copies of 27
18151. .18287
  /note="AluJo
52255. .52557
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42702. .4303
                                                                                                                                                                                                                                                                                                               /note="AluY repeat: matches 301 42255, 42299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27487. .27787
/note="Alusg repeat: matches 297. .1 of
28466. .28524
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                                                                                                                                /note="AluY repeat:
                                                                                                                                                             /note="MIR repeat: matches 7. .203 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                               /note="MER33 repeat: matches 9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MER20 repeat: 34906. .35188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30980. .3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MIR repeat; matches 257, .195 of consensus" 28538, .28843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MIR2 repeat: matches 146.
28475. .28537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Tn10 flanking repeat; Tn10 sequence was inserted at position 21992. 21993; in some sequenced clones which were
                                                                                                                                                                                                                               note="MLTlF repeat: matches 541. .300 of
                                                                                                                                                                                                                                                                 note-"MER1B
                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluSq repeat:
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                                                                                                 .5011
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                                                                                                                                                                                                                                                                                                                                                        ctggagatcgatttgggggagaaaaagaaaataacagg 1118
                                                                                                                                                                                                                                                                                                                                                                                                                    GACCAAGGCCCATCATGGGCTTCGGGCGACAGTAGCAACCACAAACCACACAGAGTGG 51264
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                                                                                                                                                                       142616 bp
Homo saptens chromosome 6 clone
SEQUENCE, 7 unordered pieces.
ACO26646
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Butherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 142616) Waterston, R. H.
                                                                                                                                               AC026646
AC026646.5 GI:10998991
                                                                                  Homo sapiens
                                                                                                                           HTG; HTGS_PHASE1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="match: multiple ESTs; match: T24499, A069666 U82788 H11008 H21591; match: N25570 AA128011 W03600 N48006 N56225; match: R44125 R24821 N29055 N94008 N32358; match:
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AA026810 N29184 W45579"
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68690. .69515
/note-"LipH3 repeat: matches 897. .64 of consensus"
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incomplete repeat"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MIR repeat: matches 14. .250 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MIR repeat: matches 216. .116 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="AluJo repeat: matches 300. .5 of consensus"
56848. .56947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MIR repeat: matches 3. .261 of consensus"
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Pred. No. 1.5e-31;
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Chemistry: Dyc-carminator Big Dye; 0% of reads
Chemistry: Dyc-carminator Big Dye; 0% of reads
Chemistry: Dyc-carminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 119293 bases at least 030
Consensus quality: 140128 bases at least 030
Consensus quality: 140128 bases at least 030
Consensus quality: 140128 bases at least 030
Insert size: 14104, sayrose-fp
Quality coverage: 5.86 in 020 bases; sum-of-contigs
Quality coverage: 5.84 in 020 bases; sum-of-contigs
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Submitted (22-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA No. 1000 this sequence version replaced gi:9958143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: H_NH0117013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 142616)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence of Homo sapiens clone 
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Caps between the contigs are represented as runs of N, but the exact sizes of the gaps, are unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/chromosome="6"
                                                                  /note="assembly_name:Contig8" 67413. .97063
                           /note="assembly_name:Contig9
clone_end:SP6
                                                                                                              40052.
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                                                                                                                                                                                                                                    /note="assembly_name:Contig5"
11383. .20730
                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                     /note="assembly_name:Contig7
                                                                                                                                                                                                              /note-"assembly_name:Contig6"
                                                                                                                                                                                                                                                                                           /note="assembly_name:Contig4"
                                                                                                                                                                                                                                                                                                                                    clone="RP11-117013"
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contig of 27261 bp in length
gap of unknown length
contig of 29651 bp in length
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contig of 19121 bp in length
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contig of 45453
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contig of 9348 bp in length
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      Foster, P., Frantz, F., Falis, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunardoe, P., Hale, S., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunardoe, P., Hale, S., Hamlton, K., Harris, C., Harris, K., Harris, K., Harris, K., Harris, K., Harris, K., Harris, K., Harris, C., Harris, K., Hoyes, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Huly, S., Hame, J., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korysh, J., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korysh, J., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korysh, J., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korysh, J., Kovar, C., Kratovic, J., Kurcsh, A., Landry, N., Leel, B., Laus, J., Liu, J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Talfrod, B., Thomas, R., Thomas, R., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Wareren, R., Washington, S., Waltlamson, A., Wilatzik, R., Wooden, S., Waltlamson, S., Wilatzik, R., Wooden, S., Wooley, K., Wu, C., Wh, Y., Wh, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G., and Gibbs, R.
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(see http://www.lusc.bcm.tmc.edu/docs/denbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 58 contigs. The true order of the places
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                               as soon as it is available and the accession number will be preserved.
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Center project name: GHUB
Center clone name: CH230-101K6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Consensus quality: 147464 bases at least 030
Consensus quality: 155580 bases at least 020
Estimated insert size: 152596; sum-of-contigs estimation
Quality coverage: 0x in 020 bases; agarose-fp estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Chemistry: Dye-primer Er; 100% of reads
Chemistry: Dye-terinator Big Dye; 0% of reads
Assembly program: Phrap: version 0.990319
Consensus quality: 13923 bases at least Q40
Consensus quality: 140126 bases at least Q30
Consensus quality: 140126 bases at least Q30
Consensus quality: 140126 bases at least Q30
Insert size: 141001; agarose-fp
Insert size: 142145; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tatottotottoacoagotottoagatoaatatggtocatactgtgggaagtatgactgt 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATCTCCTCTTTAGCAGTGCGACAGATCAGTATGGTAAGGAACGGGTATGGGGATCTGT 9321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC026646

Homo sepiens chromosome 6 clone RP11-117013, WORKING DRAFT SEQUENCE, 7 unordered pieces.
AC026646, GI:10998991

HTG: HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (22-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USB.
On Oct 25, 2000 this sequence version replaced gi:9958143.
                                                                                                                                                                                             Center: Washington University Genome Sequencing Center
Center code: MUGSC
Web site:http://genome.wust.edu/gsc/index.shtml
center project name: H_MI0111011
                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 142616)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 142616)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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166741:
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    Mismatches

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Pred. No. 2.
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g of 1592 bp in length
f unknown length
g of 1716 bp in length
g of unknown length
g in unknown length
if unknown length
if unknown length
if unknown length
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f unknown length
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.9e-20;
es 50; Indels
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length
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Louis,

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RESULT
HUMCUB1
      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                 15093 GCCAGATCAGTGTGCTTCAGCGCAAAGGGATCAGTCGATATGAAGGGATTCTGGCCAATG 15152
                                                                                                                                                                                                              15033 AGACCTCTTTATTGTGCAAAGCTGCCATCCATGCAGGAATAATTGCTGATGAACTAGGTG 15092
                                                                                            15153 GTGTTCTTTCGAGGGA 15168
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                                                                                                             gtgttctttcgaggga 860
                                                                                                                                                                    gccagatcagtgtgcttcagcgcaaagggatcagtcgatatgaagggattctggccaatg 844
                                                                                                                                                                                                                                                                                   135;
  Human mRNA for unknown
                  нимсивт
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality coverage: 5.86 in Q20 bases; agarose-fp Quality coverage: 5.84 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                             43950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 7 conties. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                 Conservative
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97164. .142616
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20831. .39981
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26378 c 28311 g 43375 t
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40052. .67312
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                                                                                                                                                                                                                                                                                                                                                                                                                                        clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"assembly_name:Contig9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_name:Contig8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_name:Contig7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"assembly_name:Contig5"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note-"assembly_name:Contig4"
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99.3%;
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contig of 27261 bp in length
gap of unknown length
contig of 29651 bp in length
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gap of unknown length
contig of 9348 bp in length
gap of unknown length
contig of 19121 bp in length
                                                                                                                                                                                                                                                                                              Score 134.4;
Pred. No. 1.
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product, partial cds
            1388 bp
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              mRNA
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AUTHORS
TITLE
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536 ttgagagtggatcccacatttctggccggggttttttgctgacctatgcgagcagcgacc 595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          374 aaagactgattctgaggttgggagatttggatatcgaa----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GTGATGGATGTGGACACACTGTACTAGGCCCTGAGAGTGGAACCCTTACATCCATAAACT
                                                                                                   GTCTGGGGTTGCAATCAACCATTCAATTGAATCAAAAGGCAATGAAATCACATTGCTGT
                                                                                                                                                                                                                                                                                                                                                                                       AGAGAGTTCGCATCAAATTTGGTGACTTTGACATTGAAGATTCTGATTCTTGTCACTTTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCCACAGACCTATCCCAACAGCACTGTTTGTGAATGGGAGATCCGTGTAAAGATGGGAG 120
                                                                                                                                                                           gtggaagtatgactgttcccaaagaactcttgttgaacacaagtgaagtaaccgtccgct 535
                                                                                                                                                                                                                                             ATTACTTGAGAATTTATAATGGAATTGGAGTCAGCAGAACTGAAATAGGCAAATACTGTG 240
                                                                                                                                                                                                                                                                                                                agacctgtgcttctgactatcttctcttcaccagctcttcagatcaatatggtccatact 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               581;
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Submitted (08-ARR-1994) Tatsuhiro Shibata, National Cancer Center Reserch Institute, Pathology; 1-1 Tsukiji 5 chome chooku, Tokyo, Tokyo 104, Japan (Tel:03-3542-2511(ex.4208), Fax:03-3248-2737)
2 (bases 1 to 1388)
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1-1 Tsukiji 5 chome
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(bases 1 to 1388)
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QDKITGGUNKTITTMYRNURLPPITARLLE"
a 289 c 302 g 364 t 1 others
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//db_xref="G1:704441"
//db_xref="G1:704441"
//tanslatlon="DGCGHYULGPESGTLTSINYPOTYPNSTYCEMEIRYKHGERVRI
//tanslatlon="DGCGHYULGPESGTLTSINYPOTYPNSTYCEMEIRYKHGERVRI
//tanslatlon="DGCGHYULGPISGTLTSINYPOTYPNISSYSTAPAGCLLPARISGTLTLPNS
GHYSGRETASYSUDAORSNYLFGHCIOFFNISSYSTAPAGCLLPARISGTLTLIQYF
GYRDSSPLCMAGVHAGVYSNTLGGQISYVISKGIPYRESSLANNYTSYVGHLILLQYFF
TRYSGCYCTILGMESGOBRGSSNNSITYLENTDHTQGERSNKFRKSQAERTHYRLGTDHT
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ALIGNMENTS

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KEYWORDS SOURCE RESULT AK016485 LOCUS REFERENCE REFERENCE REFERENCE VERSION DEFINITION ACCESSION AUTHORS TITLE JOURNAL MEDLINE PUBMED TITLE AUTHORS MEDLINE ORGANISM JOURNAL TITLE AUTHORS JOURNAL, PUBMED Shibaka, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashito, H., Itoh, M., Sumi, N., Ishika, T., Ratama, M., Nishiha, T., Rarada, A., Yanamoto, R., Matsunoto, H., Sakayuchi, S., Kegami, T., Kashikayi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshiki, N., Yoneda, Y., Ishikawa, T., Ogawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., Riken integrated sequence analysis (RISa) system - 384 format sequencing pipeline with 344 multicapillary sequencer sequencers. 10 (11), 1757-1771 (2000) Carninci, P., Shibata, Y., Hayatsu, N., Sugabara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Murametsu, M., and Hayashizaki, Y. Normalisation and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome, Res. 10 (10), 1617-1630 (2000) Mus muscullus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999) clone: 4931429A04. Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4931429A04:putative CUB domain containing protein, AK016485 99279253 HTC; CAP trapper. AK016485.1 GI:12855243 AK016485 11042159 10349636 (sites) (sites) (sites) insert sequence. 1924 bp mitestis cDNA, mRNA linear HTC 19-JAN-2002

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ATPIVERHLLRAHTFSTQSGYRVPGPRPTHKHSHSSGGFPPATGATQVESYQRPASPK PVGGGYDKPAASSFLDSRDPASQSQMTSGGDDGYSAPRNGLAPLNQTAMTALL"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepared by using trohalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to Rot = 10 0 and subtraction to Rot = 100.0. Second strand CDNA was prepared with the primer adapter of sequence [9]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salto, H., Salto, R., Sakal, C., Sakal, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogobe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M., and C., Mayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hara, A. Hayatsu, N., Hill, D., Hramoto, K., Hraoka, T., Hoori, F., Hume, D., Inctani, K., Ishii, Y., Itoh, H., Izawa, M., Kasukawa, T., Kuba, D., Inctani, K., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kato, H., Kwai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kato, H., Kurihara, C., Kwai, J., Kojima, Y., Konno, H., Kouda, K., Nomira, K., Kurihara, C., Kundo, T., Okado, T., O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in R: Genomic Sciences Center and Genome Science Laboratory in RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                  TSKNYPGTYPNYTYCEKITYVPKGKHLILRIGDLNESKTCASDYLLFSSATDOVEK
CGSHAMPKELLRIKNEYTYLFKSGSHISGKGFLLTFASSDHDLITCLEKSGHYEBK
YSKFCPAGCRDIAGDISGNYTGGYROTSLLCKAATHAGIITDBLGGHIKLLGSKGISH
                                                                                                                                                                                                    /protein_id="BAB30251"
/db_xref="di_1285244"
/translation="MGTGAGGPSVLALLFAVCAPLRLQAEELGDGCGHIVTSQDSGTM
                                                                                                                                                                                                                                                                                                                                                          putative CUB domain containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="testis"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
133. 1644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="4931429A04"
PLMIGTGTVARKGSTFRPMDTDTEEVRVNTEASGHYDCPHRPGRHEYALPLTHSEPEY
                                     KKGNPYVSADAQKTSCWKQIKYPFARHQSTEFTISYDNEKEMTQKLDLITSDMADYQQ
                                                                      YEGLLANGVLSRHGSLSEKRFLFTTPGMNITTVAIPSVIFIALLLTGMGIFAICRKRK
                                                                                                                                                                                                                                                                                                                         /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                           /note="data source:Pfam, source key:PF00431,
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GCGATTTCTTTTTACAACCCCAGG
                                     gcgatttctgtttacctccaatgg 902
                                                                            TCACTATGAAGGACTCCTGGCCAATGGCGTGCTCTCCCGGCATGGTTCTTTTTCCGGAAAA
                                                                                                 AGGGATCATCACAGATGAACTAGGTGGCCACATCAACTTGCTTCAGAGCAAAGGGATAAG
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AK014521 2835 bp mRNA linear HTC 19-JAN-2002 Mus musculus 0 day neonate skin CDNA, RIKEN full-length enriched

library, clone:4631413K11:putative CUB domain containing protein.

HTC; CAP trapper Mus musculus (st AK014521.1 GI:12852430

musculus (strain:C57BL/6J) 0

day neonate skin

CDNA

to mRNA

AK01452

insert

sequence.

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Shibata,K., Itoh,M., Alzawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Ronno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishi,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Natsunoto,H., Sakaguchi,S., Ikegani,T., Kashiwayi,K., Fujiwake,S., Inoue,K., Togawa,Y., Taawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,Y., Taawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,X., Tanaka,T., Matahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,X., Tanaka,T., Matahiki,M., Natahiki,M., Thoue,Y., Kira,A. and Hayashizaki,Y. RikeN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer 25339212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Bromstein, M., Bult, C., Carninci, P., Frkuda, S., Fakunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, M., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishili, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Konno, H., Kouda, M., Koya, S., Kato, H., Kawai, J., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Myazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Salto, H., Saito, R., Sakai, C., Saho, H., Sasaki, D., Salto, H., Salto, R., Sakai, C., Saho, H., Sasaki, D., Shinata, Y., Shinagawa, A., Shiraki, T., Shinata, K., Shinagawa, A., Shiraki, T.,
                           prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 10.0 . Second strand cNA was **constant.
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clone:4631413K11.
                                                                                                                                    Exploration Research Group. RIKEN Gemomic Sciences Center (GSC).
RIKEN Yokohama Institute; 1 7-22 Suehiro-cho, Tsurumi-Ku, Yokohk
Kanagawa 230-0045, Japan (E-mailigenome-reségscriken.go.)p,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sogaba, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraties for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                                                            cDNA library was prepared and sequenced in Mouse Genome 
Encyclopedia Project of Genome Exploration Research Gro
                                                                                                                                                                                                                                                                                                                                      Please visit our web site (http://genome.gsc.riken.go.jp/)
                                                                                                                                                                                                                                                                                                                                                                             URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222
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5 (bases 1 to 2835)
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High-efficiency full-length cDNA cloning
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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adapter of sequence
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strand cDNA was prepared with [5'
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PUBMED

JOURNAL MEDLINE

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AUTHORS JOURNAL AUTHORS

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REFERENCE

AUTHORS

MEDLINE PUBMED

JOURNAL TITLE AUTHORS REFERENCE

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226 ccgctccggctgcaggcggaggagctgggtgatggctgtggacacctagtgacttatcag 285
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gaatacagcaaattotgcccagctggttgtagagacgtagcaggagacatttotgggaat
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                                                                                       AGCAGTGACCATCCAGATTTAATAACCTGTTTGGAACGAGGCAGCCATTATTTCGAGGAA
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/db_xref-"g1:12859411"
/db_xref-"g1:12859411"
/translation-"MYSKNYPGYYPNYTYCEKIITVPKGKRLILRLGDLNIESKTCAS
DYLLFSSAYDOYGPYGCSMAVPKELELMSNEWYFVLEKGGSHISGRETLLTYASSDED
LITCLERGSHYEBEKYSKFCPAGCEDIAGDISGNYKFOYFOYSILCKAAHAGIITDE
LGGHINLLQSKGISHYEGLLANGVLSRHGSLSEKRFLFTTPGMNITTVAIPSVIFIAL
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/clone_lib="RIKEN full-length enriched mouse
/dev_stage="0 day neonate"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="4631413K11"
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Tissue Procurement: Gilbert Smith, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chozdata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 872)
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Plate: LLAM10331 row
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National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)4
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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Location/Qualifiers
                                                                                                                                                                                                      /note="Organ: mammary; Vector: pCMY-SFOKTb
Site_2: Not1; Cloned unidirectionally. Pr
Library constructed by Life Technologies.
providing samples: Gilbert Smith, NIH"
a 202 c 249 g 208 t
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/clone_llb="NCI_CGAP_Maml"
/tissue_type="tumor_biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
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SOURCE REFERENCE VERSION KEYWORDS ACCESSION JOURNAL TITLE AUTHORS Eukaryota; Metazoa; Chordata; Cr Mammalia; Eutheria; Rodentia; Sc 1 (bases 1 to 883) NIH-MGC http://mgc.nci.nih.gov/ Unpublished (1999)
Contact: Robert Strausberg, Ph.D. National Institutes of Health, Mammalian Mus musculus BG975603.1 GI:14363240 BG975603 house mouse. Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus Gene Collection

Ph.D

Tissue Procurement: Lothar Hennighausen Ph.D.,

Priscilla

Furth

CDNA Library Preparation: Life Technologies, CDNA Library Arrayed by: The I.M.A.G.E. Cons

Consortium

(LLNL)

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DNA Sequencing by: Incyte Genomics, Inc. Clone distribution information can Clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:

Email: cgapbs-r@mail.nih.gov

DEFINITION

mRNA sequence

BG975603

602845306F1 NIH_CGAP_Mam4 Mus

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musculus cDNA clone mRNA

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/tissue_type="tumor, gross tissue"
/lab_host="DH10B"
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Seq primer: puc 18 forward
Seq primer: puc 18 forward
High quality sequence start: 26
High quality sequence stop: 204.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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RC4-ST0185-131099-011-c01
AW390343
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4396
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 11 (4),
21180013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Casas, E., Wray, J.E., White, J., Cho, J., Pahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W. M., Rohrert, G.A., Chitko-McKown, C.G. Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Borora: Boyoldea
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AM483656 ARC 1507 BOS TAURUS CDNA
AM483656.1 GI:7053762
EST.
                                                                                                                                                                                                                                                                                                                                                                    FORWARD: AGGAAACAGCTATGACCAT BACKWARD: GTTTTCCCAGTCACGACG Plate: 28 row: E column: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
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                                                                                                                                   102
                    Conservative
                                                                                                                                 /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XboI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
1 93 c 128 g 111 t
                                                                                                                                                                                                            /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                  /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
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Pred. No. 8.9e-66;
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                                                                                                            Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project, This entry can be seen in the following UBL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1-RC26t2-RC2-HB0006-
051200-011-B078t5-2000-12-05664-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 406)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,N. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., bucher,P., Jogeneek,C.V., O'Hare
"M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   434
                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 an
                                                                                                                                                                                                                                                                                                                                                                                         sequence tags
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BF740455.1 GI:12067131
                                                                                          Seq primer: puc 18 forward
                                                                                                                                                                                                                                   Tel: +55-11-2704922
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                                                   quality sequence start: 47 quality sequence stop: 406
/organism-"Homo sapiens"
                                 Location/Qualifiers
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FEATURES

High quality sequence stop:
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                                                                                                                                                                                                                                                                               Mus muscullus Eukaryota; Merkazos; Chordata; Craniata; Vert Mammalia; Eutheria; Rodentia; Sciurognathi; 1 (bases 1 to 975)
                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                      BF144325.1
EST.
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by The I. M. A.G.E. Consortium (LLNL)
DNA Sequencing by:Inoyte Genomics, Inc.
Clone distribution: NCI-GGAP clone distribution informatifound through the I.M.A.G.E. Consortium/LLNL at:
http://lmays.llnl.gov
Plate: LLM9329 row: h column: 11
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Site_2: Sall; transgenic model NNT-1, expression dri
MNTV-LTR enhancer; Cloned unidirectionally. Primer
dT. Library constructed by Life Technologies.
Investigator providing samples; Gilbert Smith, NIH"
a. 240 c. 299 g. 188 t.
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/lab_host="DH10B"
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/clone="IMAGE:4014778"
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/strain="CZECH II"
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             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                 Homo sapiens
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
                                                                 human
                                                                                                   BF331266
BF331266.1
                                                                                                                                   BF331266 260 bp mRNA linear MRO-BT0374 Homo sapiens cDNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-6t2-MR0-BT0374-220
300-001-f076t3=2000-03-226t4-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence tags
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  (bases 1 to 260)
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Location/Qualifiers
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48 c 60 g 62 t
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/db_xref="taxon:9606"
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Pred. No. 9.5e-44;
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Query Match
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Naggi, M. A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G. H., Carvalho, A.F., Metsikuma, A., Baia, G. S., Simpson, D. H.,
Brunstein, A., deolivetia, P. S., Bucher, P., Jongeneel, C. V., O'Hare
M.J., Soures, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                mj12el0.rl Soares mouse embryo NbMEl3.5 14.5 Mus musculus CDNA clone IMAGE:475914 5', mRNA sequence.
                      AA050442
                                                                                                     AA050442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.ludwid.org.br/scripts/gethtml2.pl?ti-wR04t2-wR0-B70374-
220300-001-h014t3-2000-03-224t4-1)
Seq primer: puc 18 forward.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Smo Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence tags
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AA050442.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="Adult" // dev_stage="Adult" | Stite_1: Smal; Site_2: // note="Organ: breast: Vector: pucl8; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (US 1. Letters Batent application No. 196 / 196 | Institute for Cancer Research) profiles into the pUC 18 vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="BT0374"
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                                                                                                  TGTGTGTGAAAAGATCATCACAGTCCCAAAGGGGAAGAGACTTATTCTGAGGTTGGGAGA
                                                                                                                                                     tgtttgcgaaaagacaattacagtaccaaaggggaaaaagactgattctgaggttgggaga 398
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Miliae; Mus.

Marra M., Hillier L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Gelsei, S., Kucaba, T., Lacy, H., Le, M., Marrin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Materstoon, R.,

Marra M., Miller, L., Lennon, G., Soares, B., Wilson, R. and
Materstoon, R.,

Marra M., Miller, M., Marrin, M., Marrin, R., Milson, R. and
Materstoon, R.,

Marra M., Miller, M., Lennon, G., Soares, B., Wilson, R. and
Materstoon, R.,

Marra M., Miller, M., Marra M., Miller, M., Miller,
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4444 Forest Park Parkway, Box 8501, St. LA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: -28Ml3 rev2 from Amersham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
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/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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/clone="IMAGE:475914"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,p., Shibata, Y., Hayatsu, M., Sugahara, Y., Shibata, K.,
M., Konno, H., Okazaki, Y., Muzamatsu, M. and Hayashizaki, Y.,
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encyclopedia: real-time sequence clustering for construction of a nonredundant cDNN library. Genome Res. 11 (2), 281-289 (2001) please visit our web site (http://genome.gsc.riken.go.jp) for
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RIKEN Integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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Tel: 81-45-503-9222
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                                                                                                                                                                                                                                                                                                                       Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Sliva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsokuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RC3-HT0230-150900-112-f10 HT0230 Homo sapiens cDNA,
BF086926
BF086926.1 GI:10892636
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 451)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF086926
Contact: Simpson
                                                                                  Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                     sequence tags
                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                           M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (cell_line=RCB-0.59 k-1 . Ft), (cell_line=RCB-1.28 Hids melanoma), (cell_type=B cells, cell_line=CRL-7.02 WEHI 231 ), (cell_type=Leydig cells, cell_line=CRL-2.05 MLTC-1), (cell_type=Leydig cells cell_line=CRL-2.06 MLTC-1), (cell_type=Budletr, cell_line=CRL-2.07 ME), (tissue_type=budletr, cell_line=RCB-0.04 MET-2), (tissue_type=budletr, cell_line=RCB-0.04 MET-2), (tissue_type=Stroma cell, cell_line=RCB-0.04 Cle-H3), (tissue_type=kldney, cell_line=RCB-0.04 Cle-H3), (tissue_type=kldney, cell_line=CCB-1.04 MCB-0.04 Cle-H3), (tissue_type=kldney, cell_line=CCB-1.04 MCB-0.04 Cle-H3), (tissue_type=kldney, cell_line=CCB-1.04 MCB-0.04 Cle-H3), (strain=C3H, tissue_type=budletrine=CRL-1.04 MCB-0.04 
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Pred. No. 1.4e-38;
0; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
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SOURCE KEYWORDS VERSION Locus

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agaaaggaagtccgtatggatcagcggaggctcagaaaacagactgttggaagcagatta 1654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agatgacacaaaagttagatctcatcacaagtgatatggcaggtt 1759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aatatccctttgccagacatcagtcagctgagtttaccatcagctatgataatgagaagg 1714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAAAGGAAGTCCGTATGGATCAGCAGAGGCTCAGAAAACAGACTGTTGGAAGCAGATTA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATATCCCTTTGCCAGACATCAGTCAGCTGAGTCTACCATCAGCTATGATAATGAGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGATGACACAAAAGTTAGATCTCATCACAAGTGATATGGCAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Project. This entry can be seen in the following URL (http://www.ludwig.org/br/scripts/gethtm12.pl?tl=st2=rc3-HT0230-150 900-112-flost=2000-09-554.4-1) seen primer: puc 18 forward High quality sequence start: 14 High quality sequence stop: 451.
                                                                                     Marra,M., Hillier,L., Allen,M., Bowles,M., Districh,N., Dubuque.T
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoce,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                             AA042037 406 bp mRNA linear EST 03-SEP mj04h12.rl Soares mouse embryo NbMEl3.5 14.5 Mus musculus CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Brazil
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Ludwig Institute for Cancer Research
Unpublished (1996)
Contact: Marra M/M
                                               The WashU-HHMI Mouse EST Project
                                                                      Waterston, R.
                                                                                                                                                                             Mammalia; Eutheria;
1 (bases 1 to 406)
                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                 Mus musculus
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                                                                                                                                                                                                                                                                                                                                                           clone IMAGE: 475175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Organ: head_neck; Vector: pucl8; Ste_1: Smal; site_2: Smal; A mini-library was made by cloaning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0230"
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     M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                           5', mRNA sequence
                                                                                                                                                                                                     Chordata;
Rodentia;
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Pred. No. 3.9e-35;
0; Mismatches 8
                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                    356
                                                                                                                                                                                                                                                   399 tttggatatcgaatcccagacctgtgcttctgactatcttctcttcaccag 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116
                                                                                                                                                                                                                                                                                                                                                                                       236 CTCTCAGGACAGTGGCACAATGACATCTAAGAATTATCCAGGGACTTACCCCAATTACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 ctccgccccgctccggctgcaggcggaggagctgggtgatggctgtgggacacctagtgac 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                 TTTGAACATTGAGTCCAAGACCTGCGCTTCTGACTATCTCCTCTTCAGCAG 406
                                                                                                                                                                                                                                                                                                           TGTGTGTGAAAAGATCATCACAGTCCCAAAGCGGAAGAGACTTATTCTGAGGTTGGGAGA
                                                                                                                                                                                                                                                                                                                                tytttgcgmamagacmattacagtaccmamaggggmamagactgattctgmggttgggmaga 398
                                                                                                                                                                                                                                                                                                                                                                                                            ttatcaggatagtggcacaatgacatctaagaattatcccggggacctaccccaatcacac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCCGGGACCATGTGGACCGGGGCTGGTGGGGGCCGAGTGTCCTGGCGGTGCTGCTGTTCGCCGT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240;
                                  mRNA sequence.
BF139411
BF139411.1 GI:10978451
EST.
                                                                                                        BF139411 896 k
601785285F1 NCI_CGAP_Lu30 Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mousest@watson.wustl.edu
Email: mousest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO
house mouse.
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: -28M13 rev2 from Amersham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence stop: 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="unknown'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Soares mouse embryo NbMEl3.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="IMAGE:475175"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="C57BL/6J"
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Pred. No. 1.5e-34;
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t
                                                                                                                                   mRNA
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                                                                                                              A linear EST 24-OCT-2000 CDNA clone IMAGE:4013276 5',
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ORIGIN
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                            1489 acatccacaggaatasacattacaacggtggctattccattggtgctccttgttgttcttg 1548
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Plate: LLAM9255 row: i column: 21
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Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) CDNA Sequencing by:Incyte Genomics, Inc. Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 a
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/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
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/db_xref="taxon:10090"
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000
         /cgn2_6/ptodata/72/ina/5a_COMB.seq:*
/cgn2_6/ptodata/2/ina/5b_COMB.seq:*
/cgn2_6/ptodata/2/ina/6a_COMB.seq:*
/cgn2_6/ptodata/2/ina/6a_COMB.seq:*
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US-08-474-593-1

US-08-670-707A-1

US-90-337-601-1

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	Sequence 11, Appl				38,	ហ			Sequence 5, Appli	7, 1	•	•	42	Sequence 7, Appli	٢	Sequence 1, Appli	Sequence 9, Appli	Sequence 9, Appli-	

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; MOLECULE TYPE:
US-08-804-196-1
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: INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHRANCTERISTICS:

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Patent No. 5874256
                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/804,196
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/454,353
FILING DATE: 06-UNI-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Akzo No. 5874256el Patent Department
STREET: 1300 Piccard Drive, Suite 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: A method for diagnosing an increased TITLE OF INVENTION: Tisk for thrombosis or a genetic defect of TITLE OF INVENTION: thrombosis and kit for use with the same.
                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bertina, Rogier APPLICANT: Reitsma, Pieter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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E: Maryland
RY: USA
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EDNESS: both
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Score 92.8; DB 2;
Pred. No. 1.2e-13;
0; Mismatches 232;
                                     Length 6909;
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Matches 248;

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APPLICANT: Bertina, Rogier
APPLICANT: Reitsma, Pieter
TITLE OF INVENTION: A meth
TITLE OF INVENTION: risk for
TELEFAX: (301) 948-9751
INFORMATION FOR SEQ ID NO:
                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 948-7400
                                                                                                 FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gormley, Mary E.
                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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CITY: F
STATE:
                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                            NAME: Gormley, Mary E. REGISTRATION NUMBER: 34,409
                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                         ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                 Maryland
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                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                      Akzo No. 5910576 5861489el Patent Department 00 Piccard Drive, Suite 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A method for diagnosing an increased
risk for thrombosis or a genetic def
thrombosis and kit for use with the
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Best Local Similarity 51.0%;
Matches 248; Conservative
                                                                                                                                                                                                                                                                                                                                                                            Sequence 26, Application US/08746111 Patent No. 6066778
                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                            ZIP: 94104
COMPUTER READABLE FORM:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                     TITLE OF INVENTION: Compositions and Methods For Screening
TITLE OF INVENTION: Compounds For Anticoagulant Activity
NUMBER OF SEQUENCES: 54
                                                                                                                                                                                                                                                                                                               APPLICANT: Ginsburg, David
APPLICANT: Cui, Jisong
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LENGTH: 6909 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6514
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                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: unknown
                                                                                                                                   COUNTRY:
                                                                                                                                                                           STREET: 220 Montgomery Street,
CITY: San Francisco
                     SOFTWARE:
                                                                                                                                                           STATE:
                                                                                                                                                                                                                   ADDRESSEE: Medlen & Carroll,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cagatt 1383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGGAATGGAAACCATACAGGCTGAAATCCTCCATGGTGGACAAGATTTTTGAAGGAAAT 6633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tctaagtggaagacctataaaggaattgtgaataatgaagaaaaggtgtttcagggtaac 1257
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                                                                                                                                                         California
                  PatentIn Release #1.0,
                                                                                                                                   United States
                                                                                                                                      of America
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Pred. No. 1.2e-13;
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                     Version #1.30
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                                                                                                                                                                                                                                                US-09-324-867-1
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                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Lillicrap, David
APPLICANT: Cameron, Cherie
APPLICANT: Cameron, Cherie
APPLICANT: No. 6251632ley, Colleen
APPLICANT: Horrocks, L. Suzanne Hoyle
APPLICANT: Horrocks, L. Suzanne Hoyle
APPLICANT: Horrocks, L. Suzanne Hoyle
APPLICANT: Hough, Christine Factor VIII Gene, Protein and Methods of Use
FILE REFERENCE: 1669.0010002/JAG/BJD
                                                                                                                                                                                                Sequence 1, Application US/09324867A Patent No. 6251632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6280 AATGGATGTTCCACACCCCTGGGTATGGAAAAATGGAAAGATAGAAAACAAGCAAATCACA 6339
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REFERENCE/DOCKET NUMBER: UM
TELECOMMUNICATION INFORMATION:
TELEBOOME
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LENGTH: 6909 base pair
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ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              898 aatggttgcagcagatccttgagttttgaacctgacgggcaaatcagagcttcttcctca 957
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Local Similarity 51.0%;
hes 248; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 06-NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                   cgggttgtcccccagacatggcaccagaggatagccttgaaggtggagctcattggttgc 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tctaagtggaagacctataaaggaattgtgaataatgaagaaaaggtgtttcagggtaac 1257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGTCTCTGTCCTCTGAAATGTATGTAAAGAGCTATACCATCCACTACAGTGAGCAGGGA 6573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acacagtcgaacttcaacttttatgttaagagttttgtgatgaacttcaaaaacaataat 1197
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EDNESS: double
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Pred. No. 1.2e-13;
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RESULT 5
US-08-746-111-4
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; LOCATION: 1..7029
US-09-324-867-1
                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08746111 Patent No. 6066778 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 4.6%;
Best Local Similarity 54.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/324,867A
CURRENT FILING DATE: 1999-06-10
EARLIER APPLICATION NUMBER: 09/035,141
EARLIER FILING DATE: 1998-03-059
EARLIER APPLICATION NUMBER: 60/039,953
EARLIER FILING DATE: 1997-03-06
NUMBER OF SED ID NOS: 63
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                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 7032
                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: medlen & Carroll,
                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Compositions And Methods For Screening TITLE OF INVENTION: Compounds For Anticoagulant Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1354 ttgaaggtggagctcattggttgccaga 1381
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                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                            ADDRESSEE: Medien a constraint street,
                                                                                                                             COUNTRY:
  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ctgaggctggaggtcctgggctgcgaca 7015
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                                                                                                              94104
                                                                                                                                                    California
                                                                                                                             United States
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PatentIn Release #1.0, Version #1.30
                                                                                                                                of America
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Pred. No. 7.5e-11;
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; LOCATION:
US-08-746-111-4
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                                                                                                                                                                                                                     Sequence 7, Application US/08484891 Patent No. 5935935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                  GENERAL INFORMATION:
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NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE_FOSCKET NUMBER: UN-
TELECOMMUNICATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6161 AGACTACTGGGAGCCCTCCCTTGCCCGCCTGAACGCCCAGGGCCGCGTGAACGCCTGGCA 6220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: other nucleic DESCRIPTION: /desc = "DNA"
                                                        NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                TITLE OF INVENTION:
                                                                                                                                        APPLICANT: Kaleko, Michael APPLICANT: Smith, Theodore
                                                                                                                                                        APPLICANT: Connelly, Sheila APPLICANT: Kaleko, Michael
                                                                                                                                                                                                                                                                                                                                          6515 CATCGCCCTTCGCCTAGAGCTCTTCGGCTGTGACATT 6551
                                                                                                                                                                                                                                                                                                                                                                             1347 gatagccttgaaggtggagctcattggttgccagatt 1383
                                                                                                                                                                                                                                                                                                                                                                                                                     6455 TTTCAACCCGCCCATTATTTCCAGATTTATCCGCATCATTCCTAAAACATGGAACCAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6395 CTCCATGGTGGACAAGATTTTTGAAGGAAACAGCAATACCAAGGGGCACATGAAGAACTT 6454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6335 GAGCTACAGCATCCAGTACAGTGACCAGGGTGTGGCATGGAAACCTTACCGACAGAAATC 6394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6275 GAAGGTAACGGCCATCGTAACGCAGGGCTGTAAGTCTCTGTCCTCTGAGATGTACGTGAA 6334
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Local Similarity 52.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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  STREET:
                ADDRESSEE: Carella, Byrne, Bain, Gilfillan, ADDRESSEE: Cecchi, Stewart & Olstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gaataatgaagaaaaggtgtttcagggtaactctaactttcgggacccagtgcaaaacaa 1286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207;
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  Becker Farm Road
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                                                                                                  Treatment of Hemophilia
                                                                                                                  Adenoviral Vectors for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/746,111
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Pred. No. 1.3e-10;
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NAME/KEY:
US-08-484-891-7
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RESULT 7
US-08-717-294-41
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4077
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LENGTH: 4629 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 10-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2
FILING DATE: 25-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                     1353
                                                                                                                                                                                                                                          4251
                                                                                                                                                                                                                                                                                                                          4197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1053 tagcaacaaccacaaaccacgagagtggctggagatcgatttggggggagaaaaagaaaat 1112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     993 ctggtctcctggccaagcccgacttcaggaccaaggcccatcatgggcttcgggcgacag 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
FILING DATE: 07-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/074,920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                        cttgaaggtggagctcattggttgccag
                                                                                                                                                                                                                                                                     tgaagaaaagtgtttcagggtaactctaactttcgggacccagtgcaaaacaatttcat 1292
                                                                                                                                                                                                                                                                                                                                                  tgtgatgaacttcaaaacaataattctaagtggaagacctataaaggaattgtgaataa 1232
                                                                                                                                                                                                                                                                                                                                                                                                                                        aacaggaattaggaccacaggatctacacagtcgaacttcaacttttatgttaagagttt 1172
                                                                                CCTGAGGATGGAGGTTCTGGGCTGCGAG
                                                                                                                                                          ccctcccatcgtggccagatatgtgcgggttgtcccccagacatggcaccagaggatagc 1352
                                                                                                                                                                                                                                          CAAAGTAAAGGTTTTTCAGGGAAATCAAGACTCCTTCACACCTGTGGTGAACTCTCTAGA 4310
                                                                                                                                                                                                                                                                                                                          CCTCATCTCCAGCAGTCAAGATGGCCATCAGTGGACTCTCTTTT-----TTCAGAATGG
                                                                                                                                                                                                                                                                                                                                                                                                   ACCTCAGGTGAATAATCCAAAAGAGTGGCTGCAAGTGGACTTCCAGAAGACAATGAAAGT 4136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGGTCTCCTTCAAAAGCTCGACTTCACCTCCAAGG-----GAGGAGTAATGCCTGGAG 4076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WordPerfect 5.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201-994-1700
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Pred. No. 4e-10;
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                                                                                4398
                                                                                                                     1380
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Matches 210; Conserv
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                                                  1293 ccctcccatcgtggccagatatgtgcgggttgtcccccagacatggcaccagaggatagc 1352
                                                                                                                                                               4223 CCTCATCTCCAGCAGTCAAGATGGCCATCAGTGGACTCTCTTTT-----TTCAGAATGG 4276
                                                                                                                                                                                                                                                                                                          4103 ACCTCAGGTGAATAATCCAAAAAGAGTGGCTGCAAGTGGACTTCCAGAAGACAATGAAAGT 4162
                                                                                                                      1233 tgaagaaaaggtgtttcagggtaactctaactttcgggacccagtgcaaaacaatttcat 1292
                                                                                                                                                                                              1173 tgtgatgaacttcaaaaacaataattctaagtggaagacctataaaggaattgtgaataa 1232
                                                                                                                                                                                                                                    1113 aacaggaattaggaccacaggatctacacagtcgaacttcaacttttatgttaagagttt 1172
                                                                                                                                                                                                                                                                                                                                  1053 tagcaacaaccaacaaaccaacgagagtggctggagatcgatttgggggggagaaaagagaaat 1112
                                                                                                                                                                                                                                                                                                                                                                                   4049 CTGGTCTCCTTCAAAAGCTCGACTTCACCTCCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDN/
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                      993 ctggtctcctggccaagcccgacttcaggaccaaggcccatcatgggcttcgggcgacag 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SEED, BRIAN APPLICANT: HAAS, JURGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX:
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TELEFAX: 617-428-7045
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
SOFTWARE: FastSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 20-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/717, 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Clark & Elbing LLP STREET: 176 Federal Street
                                                                                         CAAAGTAAAGGTTTTTCAGGGAAATCAAGACTCCTTCACACCTGTGGTGAACTCTCTAGA 4336
                     CCCACCGTTACTGACTCGCTACCTTCGAATTCACCCCCAGAGTTGGGTGCACCAGATTGC 4396
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Pred. No. 4e-10;
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GENERAL INFORMATION:
APPLICANT: Couto, Linda B.
                                    Sequence 14, Application US/09364862 Patent No. 6221349
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; OTHER INFORMATION: Description of Artificial Sequence: US-09-470-618-14
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Matches 210; Conserv
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APPLICANT: COLDSI, Peter C.
TITLE OF INVENTION: Adeno-Associated Vectors for Expression of Factor VIII
FILE REFERENCION: by Target Cells
FILE REFERENCE: Avigen-0405
CURRENT APPLICATION NUMBER: US/09/470,618
CURRENT PRILIG DATE: 1959-07-36
EARLIER FILING DATE: 1959-07-36
ARKLER FILING DATE: 1959-07-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: 60/104,994 EARLIER FILING DATE: 1998-10-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                        1353 cttgaaggtggagctcattggttgccag 1380
                                                                                                                                                                                                                                                                                                                                                                                                           1113 aacaggaattaggaccacaggatctacacagtcgaacttcaacttttatgttaagagttt 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4450 acctcaggtgaataatccaaaagagtggctgcaagtggacttccagaagacaatgaaagt 4509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4396 ctggtctccttcaaaagctcgacttcacctccaagg-----gaggagtaatgcctggag
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                                                                                                                                                                                                                                                                                                                                                           1173 tgtgatgaacttcaaaaacaataattctaagtggaagacctataaaggaattgtgaataa 1232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                993 ctggtctcctggccaagcccgacttcaggaccaaggcccatcatgggcttcgggcgacag 1052
cctgaggatggaggttctgggctgcgag
                                                                                                                            ccctcccatcgtggccagatatgtgcgggttgtcccccagacatggcaccagaggatagc 1352
                                                                                                                                                                                                  caaagtaaaggtttttcagggaaatcaagactccttcacacctgtggtgaactctctaga 4683
                                                                                                                                                                                                                                                         tgaagaaaaggtgtttcagggtaactctaactttcgggacccagtgcaaaacaatttcat 1292
                                                                                                                                                                                                                                                                                                          cctcatctccagcagtcaagatggccatcagtggactctctttt-----ttcagaatgg 4623
                                                                                             cccaccgttactgactcgctaccttcgaattcacccccagagttgggtgcaccagattgc
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Pred. No. 4.1e-10;
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US-08-882-083-1
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EARLIER FILING DATE: 1999-03-24
EARLIER PILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIA VET. 2.0
SEQ ID NO 14
SEQ ID NO 16
SEQ I
                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application Patent No. 5869292
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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TITLE OF INVENTION: ADENO-ASS
TITLE OF INVENTION: BY TARGET
TITLE OF INVENTION: CELLS
FILE REFERENCE: AVIGEN-03743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/364,862
CURRENT FILING DATE: 1999-07-30
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ORGANISM: Artificial Sequence
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                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                 CITY: Washington
COMPUTER:
                                                                                                           COUNTRY: USA
                                                                                                                                              STATE:
                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                    20007-5109
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IBM PC compatible
                                                                                                                                                                                                                           Foley & Lardner
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Pred. No. 4.1e-10;
                                                                                                                                                                                                    Suite 500
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Best Local S
Matches 210
                                                                                                                                                                                                Sequence 1, Application US/08558107
Patent No. 5910481
                                                                                                                                                                     GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/882,083
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMUNICATION INFORMATION: TELEPHONE: (202)672-5300 TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                         CORRESPONDENCE ADDRESS:
                                                                                    APPLICANT: VOORBERG, Johannes J.
TITLE OF INVENTION: HYBRID PROTEINS WITH
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                             4975 CCTGAGGATGGAGGTTCTGGGCTGCGAG 5002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
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les 210; Conserv
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                              ADDRESSEE:
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Pred. No. 4.1e-10;
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       Suite
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                                                                                                                   MODIFIED ACTIVITY
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US-08-558-107-1
                                                                                                    Sequence 1, Applic
Patent No. 6130203
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Matches 210; Conserv
                                 GENERAL INFORMATION:
APPLICANT: VOORBERG, Johannes J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                      4975 CCTGAGGATGGAGGTTCTGGGCTGCGAG
                                                                                                                                                                                                                                                                                                                                                            1353 cttgaaggtggagctcattggttgccag 1380
    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1233 tgaagaaaaggtgtttcagggtaactctaactttcgggacccagtgcaaaacaatttcat 1292
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LENGTH: 5035 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
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OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATCHTIN KALESSE $1.0, VETSION $1.30.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/558,107

FILING DATE: 13-NOV-1995

OTHER PROTECTION OF THE PROTECTION AND TH
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       993 ctggtctcctggccaagcccgacttcaggaccaaggcccatcatgggcttcgggcgacag 1052
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D.C.
                                                                                                                                          Application US/09243539
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HYBRID PROTEINS WITH MODIFIED ACTIVITY
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Pred. No. 4.1e-10;
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SEQUENCE CHARACTERISTICS:
LENGTH: 5035 base pairs
  4975
                                                                                                                                                               1233 tgaagaaaaggtgtttcagggtaactctaactttcgggacccagtgcaaaacaatttcat 1292
                                                                                                                                                                                                                                 1173 tgtgatgaacttcaaaaacaataattctaagtggaagacctataaaggaattggtgaataa 1232
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US 0:
FILING DATE: 13-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             993 ctggtctcctggccaagcccgacttcaggaccaaggcccatcatgggcttcgggcgacag 1052
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TELEFAX: 904136
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Local Similarity 54.1%;
hes 210; Conservation
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TOPOLOGY: li
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
CCTGAGGATGGAGGTTCTGGGCTGCGAG
                             cttgaaggtggagctcattggttgccag
                                                                   CCCACCGTTACTGACTCGCTACCTTCGAATTCACCCCCAGAGTTGGGTGCACCAGATTGC
                                                                                                   ccctcccatcgtggccagatatgtgcgggttgtcccccagacatggcaccagaggatagc 1352
                                                                                                                                       CAAAGTAAAGGTTTTTCAGGGAAATCAAGACTCCTTCACACCTGTGGTGAACTCTCTAGA
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Pred. No. 4.1e-10;
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US-08-276-594A-
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Best Local
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INFORMATION FOR SEQ ID NO:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PATENTIN Release #1.0
CURRENT APPLICATION NUMBER: U$/08/276,5'
FILING DATE: 18-JUL-1994
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
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APPLICANT: WASUDA, KENICHI
TITLE OF INVENTION: FRACTOR VIII PROTEIN COMPLEX
TITLE OF INVENTION: FACTOR VIII PROTEIN COMPLEX
          6780 CCTCATCTCCAGCAGTCAAGATGGCCATCAGTGGACTCTCTTTT-----TTCAGAATGG 6833
                                                                                           6660 ACCTCAGGTGAATAATCCAAAAGAGTGGCTGCAAGTGGACTTCCAGAAGACAATGAAAGT 6719
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/950,191
FILING DATE: 24-SEP-1992
PRIOR APPLICATION DATA: APPLICATION WAREA: JP 243262/1991
FILING DATE: 24-SEP-1991
ANTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                              1173 tgtgatgaacttcaaaaacaataattctaagtggaagacctataaaggaattgtgaataa 1232
                                                                                                                             1113 aacaggaattaggaccacaggatctacacagtcgaacttcaacttttatgttaagagttt 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 6999 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 25,258
                                                                                                                                                                                                                                                                                                                                210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Application US/08276594A 5693499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20007-5109
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TAJIMA, Yoshitaka
                                                                                                                                                                                                                                                                                                                                Conservative
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Pred. No. 4.7e-10;
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US-08-121-202-1
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                                              Matches
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                                                                                                                                                                                                                                                                                                                              TELEFAX: (617) 876-58: INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Pittman, Debra
APPLICANT: Rehemtulla, Alnawaz
APPLICANT: Wozney, John M.
APPLICANT: Kaufman, Randal J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6894
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                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
993 ctggtctcctggccaagcccgacttcaggaccaaggcccatcatgggcttcgggcgacag 1052
                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 31
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0
FILING DATE: 14-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                             Local Similarity
                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Meinert, M. C.
NAME: Meinert, M. C.
1,544
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STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTGAGGATGGAGGTTCTGGGCTGCGAG
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EDNESS: single
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                                                                Score 78.4;
Pred. No. 4
                                                Mismatches
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4.7e-10;
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6717 ACCTCAGGTGAATAATCCAAAAGAGTGGCTGCAAGTGGACTTCCAGAAGACAATGAAAGT 6776

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; Patent No. 5171844
; Patent No. 517184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 210
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                                             1353 cttgaaggtggagctcattggttgccag 1380
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                                                                                                                                                                                                                                                                                                                                                                                                                                         6843 cctcatctccagcagtcaagatggccatcagtggactctctttt-----ttcagaatgg 6896
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APPLICATION NUMBER: US
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nes 210; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 10-JUN-1988
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cctgaggatggaggttctgggctgcgag 7044
                                                                                                                                            cccaccgttactgactcgctaccttcgaattcacccccagagttgggtgcaccagattgc
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Pred. No. 5.1e-10;
0; Mismatches 166;
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Search completed: July 9, 2002, 01:07:08 Job time: 5575 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd



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Run on:
                                                                                              OM protein - protein search, using sw model
                                                  July
9, 2002, 01:07:13 ; Search time 80.25 Seconds
(without alignments)
811.081 Million cell updates/sec
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Title: Perfect score: Sequence: 3052 US-09-691-344A-4 MGFGAGQRLRPVPAPRSSAE....YDNEKEMTQKLDLITSDMAG

586

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

747574 seqs, 111073796 residues

Searched:

747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database

A_Geneseq_032802:*

A_Geneseq_032802:*

| SIDSI/qogdata/geneseq/geneseqp-embl/AA1991.DAT:*
| SIDSI/qogdata/geneseq/geneseqp-embl/AA1991.DAT:*
| SIDSI/qogdata/geneseq/geneseqp-embl/AA1991.DAT:*
| SIDSI/qogdata/geneseq/geneseqp-embl/AA1991.DAT:*
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| SIDSI/qogdata/geneseq/geneseqp-embl/AA1996.DAT:*
| SIDSI/qogdata/geneseq/geneseqp-embl/AA1999.DAT:*

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

AAU00629 ,...

AAU00629 standard; Protein; 586 A

AAU00629;

29-AUG-2001 (first entry)

Novel human protein (NHP) sequence #2

Novel human protein; NHP; CUB domain; extracellular domain; gene therapy; obesity; high blood pressure; connective tissue disorder; infertility;

NHP-mediated pathway.

Homo sapiens.

W0200129219-A1

26-APR-2001

08-OCT-2000; 2000WO-US28798

ACC CARRES OF STREET CONTRACTOR C 19-OCT-1999; 99US-0160285. 18-FEB-2000; 2000US-0183583.

_9-

(LEXI-) LEXICON GENETICS INC

Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B, Sands AT;

N-PSDB; AAS00614. WPI; 2001-290917/30

Novel nucleic acid encoding human CUB-domain containing protein, useful for drug screening, diagnosis and treatment of physiological disorders

Novel

human

protein (NHP) sequence

*3

(first entry)

AAU00630;

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                                  eaqktdcwkqikypfarhqsaeftisydnekemtqkldlitsdmag 586
                                                                  EAQKTDCWKQIKYPFARHQSAEFTISYDNEKEMTQKLDLITSDMAG 586
                                                                                                nfrdpvqnnfippivaryvrvvpqtwhqrialkveligcqitqgndslvwrktsqstsvs
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                                                                                                                                                                                                     NFRDPVQNNFIPPIVARYYRVVPQTWHQRIALKVELIGCQITQGNDSLVWRKTSQSTSVS
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Pred. No. 5.7e-265;
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RESULT
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AAU00630

standard;

Protein;

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181 228

vagdisgnmvdgyrdtsllckaaihagiiadelggqisvlqrkgisryegilangvlsrd VAGDISGNMVDGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRYEGILANGVLSRD

240

168 121

LLLNTSEVTVRFESGSHISGRGFLLTYASSDHPDLITCLERASHYLKTEYSKFCPAGCRD

lllntsevtvrfesgshisgrgflltyassdhpdlitclerashylkteyskfcpagcrd

180

120

60 107

TYPNHTVCEKTITVPKGKRLILRLGDLDIESQTCASDYLLFTSSSDQYGPYCGSMTVPKE 167

108 61

Local Similarity

Conservative

0;

Indels

0;

Gaps

0

48 ۳

mvpgargggalaraagrgllalllavsaplrlgaeelgdgcghlvtyqdsgtmtsknypg MYPGARGGGALARAAGRGLLALLLAVSAPLRLQAEELGDGCGHLVTYQDSGTMTSKNYPG

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Query Match
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                                                                                                                                                                                                    as hybridisation probes for screening libraries and assessing quene patterns. NIP nucleotide sequences are useful for detecting mutant or inappropriately expressed NIPs (for example, those proteins associated with obesity, high blood pressure, connective tissue disorders and infertility) for the diagnosis of a disease. The polynucleotides may also be used in screening for drugs effective in the treatment of symptomatic or phenotypic manifestations of perturbing the normal munction of NIP in the body. Nucleotide constructs encoding NIP products are used to genetically engineer host cells to express such products in vito. These host cells allow for the identification of compounds that bind to NIP receptors or trigger NIP-mediated pathways.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents a novel human protein (NHP) containing a CUB domain (an extracellular domain). CUB proteins have been associated with regulating development, modulating cellular processes and preventing infectious disease. NHP nucleotide sequences are useful for gene therapy of physiological disorders or diseases. NHP pilgonucleotides are useful
                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acid encoding human CUB-domain containing protein, useful for drug screening, diagnosis and treatment of physiological disorders or diseases -
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Score 2818; DB 22;
Pred. No. 5.2e-244;
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connective tissue disorder; infertility;
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Database: A_genese9,-032802 Ac NO: AAU00670

Claim 8; Fig 1; 263pp; English

The sequence represents human TANGO 229 polypeptide. This protein and can be similar others exhibit the ability to affect growth, proliferation, curvival, differentiation, activity, morphology, or movement/migration of, e.g. T cells and cells of the heart, liver, pancreas, placenta, compared to the lateral muscle, kidney, spleen, lymph node, peripheral compared to the proteins of the heart, liver, pancreas, placenta, combinating agents for regulating ealural processes, thus, the proteins can deliver associated nucleic acids can be used to promosticate, prevent, compared to the proteins of the protein of the proteins of the protein

Sequence 715 AA õ 밁 Ş 밁 Ş 밁 Ş В Q

301

sgdssnnhkprewleidlgekkkitgirttgstqsnfnfyvksfvmnfknnnskwktykg

IVNNEEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGCQITQGNDS 467

SGDSSNNHKPREWLEIDLGEKKKITGIRTTGSTQSNFNFYVKSFVMNFKNNNSKWKTYKG

밁

481 rkkkkgspygsaeagktdcwkqikypfarhqsaeftisydnekemtqkldlitsdmag 539

RKKKKKGSPYGSAEAQKTDCWKQIKYPFARHQSAEFTISYDNEKEMTQKLDLITSDMAG lvwrktsqstsvstkkedetitrpipseetstginittvaiplvllvvlvfagmgifaaf LVWRKTSQSTSVSTKKEDETITRPIPSEETSTGINITTVAIPLVLLVVLLVFAGMGIFAAF

480

07-SEP-2001

229 polypeptide. (first entry) AAU00670 standard; Protein; 715

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                                Matches 538;
                                      Query Match
Best Local Similarity
                48
Conservative
                                      92.1%;
                               0;
                                      Score 2812; DB 22;
Pred. No. 2.8e-243;
                                Mismatches
                                              Length
                               0;
                               Gaps
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0

õ 108 MVPGARGGGALARAAGRGLLALLLAVSAPLRLQAEELGDGCGHLVTYQDSGTMTSKNYPG 107 60

õ 밁 밁 121 168 61 lllntsevtvrfesgshisgrgflltyassdhpdlitclerashylkteyskfcpagcrd LLLNTSEVTVRFESGSHISGRGFLLTYASSDHPDLITCLERASHYLKTEYSKFCPAGCRD 227

Human: TANGO 229, T cell; heart; liver; pancreas; placents; brain; lung; skeletal muscle; kidney; spleen; lymph node; peripheral blood celkocyte; bone marrow; thymus tissue; abnormal blood coagulation; asthma; cancer; banephylaxis; hepatitis; multiple sclerosis; coordnary artery disease; malaria; atopic dermatitis; amyorrophic lateral sclerosis; menlitis; attention deficit disorder; Crohn's disease; gastroenteritis; gpitre; hypodycaemia; diabetes mellitus; endometricisis; pulmonary embolism;

muscular dystrophy;

immuno-competence; vertebrate;

pulmonary embolism; e; blood; serum.

õ 당 181 228 VAGDISGNMVDGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRYEGILANGVLSRD 287 240

Ş 288 GSLSDKRFLFTSNGCSRSLSFEPDGQIRASSSWQSVNESGDQVHWSPGQARLQDQGPSWA 347 300

õ 밁 348 241

밁 301 sgdssnnhkprewleidlgekkkitgirttgstqsnfnfyvksfvmnfknnnskwktykg SGDSSNNHKPREWLEIDLGEKKKITGIRTTGSTQSNFNFYVKSFVMNFKNNNSKWKTYKG

밁 Q

468

밁 421 RKKKKKGSPYGSAEAQKTDCWKQIKYPFARHQSAEFTISYDNEKEMTQKLDLITSDMA 585

481 rkkkkkgspygsaeaqktdcwkqikypfarhqsaeftisydnekemtqkldlitsdma

AAU00628

AAU00628; Protein; 487

29-AUG-2001

(first entry)

2001-308477/32 AAS00660

Mackay CR,

Myers PS,

Kirst SJ,

Fraser CC,

(MILL-) MILLENNIUM PHARM INC

99US-0420707

23-JUN-2000; 2000WO-US17386

WO200129088-AJ

/note= 481..715 456..480

"Cytoplasmic domain"

Doma in

Protein

/note= "Mature human TANGO 229"

/note= "Extracellular domain"

/note= "Transmembrane domain"

Doma in

Peptide Homo sapiens

/note= "Signal peptide' Location/Qualifiers

New isolated nucleic acid molecule for diagnosis, prevention, and therapy of human and other animal disorder, or as modulating agent for regulating cellular processes

Novel human protein; NHP; CUB obesity; high blood pressure;

human

protein

(NHP)

NHP-mediated pathway.

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us-09-691-344a-4.rag
                               SEQ ID NO; A
AC. NO: AAB19126, Databage: A-Genesey-032802
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Of the sequence represents a novel human protein (NHP) containing a CUB domain (an extracellular domain). CUB proteins have been associated with crequiating development, modulating cellular processes and preventing CC infectious disease. NHP nucleotide sequences are useful for gene therapy CC of physiological disorders or diseases. NHP oligonucleotides are useful CC as hybridisation probes for screening libraries and assessing gene patterns. NHP nucleotide sequences are useful for detecting mutant or impropriately expressed NHBs (for example, those proteins associated CC impropriately expressed NHBs (for example, those proteins associated CC with obesity, high blood pressure, connective tissue disorders and infertility) for the diagnosis of a disease. The polynucleotides may also be used in screening for drugs effective in the treatment of symptomatic CC or phenotypic manifestations of perturbing the normal function of NHP in CC genetically engineer host cells to express such products are used to constructs encoding NHP products are used to be constructs encoding NHP products are used to constructs encoding NHP products are used
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                                                                                                                                                                                                                                      FCPAGCRDVAGDISGNMVDGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRYEGIL
                                                                                                                                                                                                                                                                                                                                                                                                                 MTSKNYPGTYPNHTVCEKTITVPKGKRLILRLGDLDIESQTCASDYLLFTSSSDQYGPYC 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NHP-mediated pathways.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nehls M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 2557; DB 22; J
%; Pred. No. 1.2e-220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain; extracellular domain; gene therapy;
connective tissue disorder; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Friedrich G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 487;
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             The present sequence represents a polypeptide sequence which is isolated from lymph node stromal cells of fan /- mice. The polynucleotides and their polypeptides are useful for treating an inflammatory disorder, disorder of immune system and cancer selected from epithelial, lymphoid, myeloid, stromal and neuronal cancers, a viral disorder, in particular HIV infection and for modulating the growth of blood vessels. The polypeptides are useful for treating a tumour necrosis factor (TMF) mediated disorder, such as those selected from arthritis, inflammatory bowel disease and cardiac failure and a libroblast growth factor-mediated disorder. It is also useful in assays to determine biological activity, to raise antibodies, to isolate corresponding ligads or receptors, to quantify levels of protein or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 20
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                    Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Polyapptide expressed in mammalian fsn '/- lymph node stromal cells, useful for modulating growth of blood cells, for treating inflammatory and tumour necrosis factor mediated disorders, cancer and vital
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murison
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lymph node stromal cell; fsn -/- mice; inflammatory disorder; immune system disorder; cancer; viral disorder; arthritis; blood vessel growth; tumour necrosis factor disorder; arthritis; inflammatory bowel disease; fibroblast growth factor-mediated disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB19126;
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99US-0383586
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19-OCT-1999; 99US-0160285 18-FEB-2000; 2000US-0183583

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(LEXI-) LEXICON GENETICS INC

2001-290917/30

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Turner CA,

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160 61

Matches 487;

Conservative

Local Similarity

83.8%; 100.0%;

Sequence

487

or trigger

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241

QDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTTGSTQSNFNFYVKSFVMNFKNNN angvlsrdgslsdkrflftsngcsrslsfepdgqirassswqsvnesgdqvhwspgqarl

399

cognate corresponding ligand or receptors, as antiinflammatory agents

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RESULT AAG75450
XX AAG7
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                               03-NOV-1999
                                                   29-SEP-1999;
                                                                                                                                                                                                           WO200122920-A2
                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                           Human; colon cancer; colorectal carcinoma
                                                                                                                                                                                                                                                                                                                                                                                       Human colon cancer antigen protein SEQ ID
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50.9%; Pred. No. 6.9e-108;
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                                                                                                                                                                                                                                                                                                                                   cancer antigen; diagnosis;
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                                                                                                                                                                                                                                                                                                                                       detection;
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expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. Add37196 to make the present sequences used in the exemplification of the research terrories.
                                                                                                                                                                                                                                                                                                                                         cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene thorapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P
Sequence
                                          N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), wher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 7657-7660; 9803pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful for preventing,
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      583 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {\tt apawaalplsrslppcsnsssfsmplfillilvllllledagaqqqddgcghtvlgpesgt}
iamkmellgcqfipkgrppkltqpppprnsnd----lknttappkiakgrapkftqplqp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MTSKNYPGTYPNHTVCEKTITVPKGKRLILRLGDLDIE-SQTCASDYLLFTS----SSDQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                a coaquiation cofactor which is selectively expressed in hammatopoletic, heart and reproductive tissues. It has hammatatic and cerebroprotective activities. The FBH contains a Factor 5/8 signature and is useful as a therapeutic for treating coaquiation related diseases such as haemophilia and stroke. The nucleic acid is useful as hybridisation probe and amplification primer for detecting deficiencies in the level of FBH mRNA, for screening FBH gene mutations and for monitoring regulation of gene expression. Fragments of the nucleic acid are also useful as diagnostic probes and primers, and can be used in screening methods such as those using DNA chips. The present sequence is also useful as a target to screen therapeutically useful modulators of the FBH.
                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      of the F8H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a human Factor 8 homologue (F8H),
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                                                                                               178 RFESGSHISGRGFLLTYASSDHPDLITCLERASHYLKTEYSKFCPAGCRDVAGDISGNMV 23:
                                                                                                                                                                                                  124 GKRLILRLGDLDIE-SQTCASDYLLFTS----SSDQYGPYCG-SMTVPKELLLNTSEVTV 177
238 DGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRYEGILANGVLSRDGSLSDKRFLF 29;
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coagulation related disorder;
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Query Match
                                                                                                                                                                                                                      The present invention describes a recombinant soluble neuropillin (I) The present invention describes a recombinate soluble neuropillin (I) comprising an amino acid sequence in which the cell membrane-penetrating region and/or the intracellular region is deleted from a mouse-derived
                                                                        Sequence
                                                                                                                      sequence
                                                                                                                          human bloreactions and disease conditions. The present sequence represents a specifically claimed soluble neuropillin protein sequence from the present invention.
                                                                                                                                                                                               neuropillin. The soluble neuropillin can be used for the elucidation
                                                                                                                                                                                                                                                                                                                         Claim 5; Page 13-17; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                              used to
                                                                                                                                                                                                                                                                                                                                                                                                  Soluble neuropillin having a deleted cell membrane-penetrating region,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-658506/64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soluble neuropillin sNP-2 protein sequence SEQ ID NO:4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242
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                                                                                                                                                                                                                                                                                                                                                                              diagnose human disease conditions
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   Score 353.5;
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Matches 120; Conser
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                         WPI; 1999-132446/11.
N-PSDB; AAX08417.
                                                                     Ginty DD
                                                                                            (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                        17-JUL-1997;
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                                                                                                                                                                                                                                 Rattus rattus
                                                                                                                                                                                                                                                                                                                              Neuropilin-2
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 New isolated semaphorin receptor, neuropilin-2 - used to develop
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  338 RLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTTG--STQSNFNFYVKSFVMNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 TYPNHTVCEKTITVPK-GKRLILRLG-DLDIESQTCASDYLLF----TSSSDQYGPYCGS 161
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                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein; 925
                                                                   Kolodkin
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3; Mismatches 189;
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            Human secreted protein BLAST search protein
                                                                     AAB64627
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2 문 õ 밁 Ş 밁 õ 밁 Ş 믕 Ş 멅 õ 밁 õ 멅

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The neuropilins are type I transmembrane proteins and act as semaphorin III (Sema III) receptors. The semaphorins have been shown to function in repulsive axon guidance. Sema III is a screted protein that in vitro causes neuronal growth cone collepse and chemorepulsion on neurites and is required in vivo for correct sensory affected tinnervation and other aspects of development. Agents which, inhibit or enhance the interaction of a
                                                                                                                             neuro-regeneration, immune modulation including hypersensitivity and graft-rejection, and diagnosis and treatment of viral and oncological infection/diseases. The neurophilms, neurophilm-encoding nuclaic acids, and unique portions also are useful in screening chemical
                                                                                                                                                                                                                                         growth, immune responsiveness, and viral pathogenesis, and can be used in the treatment and diagnosis of neurological disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              products for the diagnosis and treatment of neurological
immunological, oncological and viral diseases
                                              genetic mapping as probes for related genes, as diagnostic reagents for genetic, neurological, immunological and oncological disease.
                                                                                                                                                                                                                                                                                               semaphorin and a neurophilin can be potent modulators of nerve
                                                                                                    libraries for regulators of semaphorin mediated cell activity, and in
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HQRIALKVELIGCQITQGNDSLVWRKTS---QSTSVSTKKEDETITRP 491
                                                                                                                                                                                                     dgrwtpqqsrlhgddngwtpnvdsn----keylqvdlrfltmltaiatqgaisretqkgy
                                                                                                                                                                                                                                                        QVHWSPGQARLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTTG--STQSNFNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         edcsknftspngtiespgfpekyphnldctftilakprmeillqfltfdlehdplqvgeg 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ieirdgdsesadllgkhcgni-apptiissgsvlyikftsdyarggagfslryeifktgs 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLF----TSSSDQYGPYCGSMTVPKELLLNTSEVTVRFESGSHISGRGFLLTY----AS
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                                                                                               yvksyklevstngedwmvyrhgknh--kvfqanndatelvlnklhtplltrfirirpqtw
                                                                                                                                                  YVKSFVMNFKNNNSKWKTYKGIVNNEEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTW 446
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Pred. No. 3.7e-22;
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Best Local S
Matches 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the human secreted proteins ABB64549-B64594. The sequence is a search result from a BLASTX homology search. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosts, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, qastrointestinal tract, liver, lung, or urogenital; (b) immune discreters e.g. Addison's disease, alterists, autoinmune haemolytic aneman, autoimmune thyroiditis, diabetes mellitus, Crobi's disease, multiple sclarosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischemias; (d) wond healing. (a) healing. (a) healing. (a) healing. (a) healing. (b) healing. (c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       healing: (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2000; 2000WO-US14934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        parasitic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI
(ROSE/) ROSEN C A.
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      260
                                                                                                                                                                                                                                                                                                                            146
                                          278 ILANGVLSRDGSLSDKRFLFTSNGCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWS
                                                                                           207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to the isolation of genes AAF32757-F32803 encoding
fsaryylvhqeplenfq----
                                                                                     dckydwldiwdgiphvgpligkycgtktpselrsstgilsltfhtdmavak
                                                                                                                               -CPAGCRDVAGDIS--GNMVDGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRYEG
                                                                                                                                                                                edcsknftspngtiespgfpekyphnldctftilakpkmeiilqflifdlehdplqvgeg
                                                                                                                                                                                                                                                                         ieirdgdsesadllgkhcgni-apptiissgsmlyikftsdyarggagfslryeifktgs 146
                                                                                                                                                                                                                                                                                                                      LLF----TSSSDQYGPYCGSMTVPKELLLNTSEVTVRFESGSHISGRGFLLTY-----AS
                                                                                                                                                                                                                                                                                                                                                                    cggrlnskdagyitspgypqdypshqncewivyapepnqkivlnfnphfeiekhdckydf 87
                                                                                                                                                                                                                                                                                                                                                                                                               CGHLVTYQDSGTMTSKNYPGTYPNHTVCEKTITVPK-GKRLILRLG-DLDIESQTCASDY 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-032312/04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 524-526; 558pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.4%; Score 349;
25.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infection; human; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Komatsoulis GA
---cnvplgmesgrianeqisassty----
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.9e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
---sdgrwt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                          RESULT
AAY06320
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                                                                                                                                                                                                                  The present sequence represents a soluble, truncated form of human neuropilin-2, a novel receptor of vascular endothelial growth factor (VEGF). The soluble neuropilin-2 deviates from the full-length protein (see AAY06318) between the b2 and c domains after amino acid 547, at the position of an exon-exon boundary, and includes 8 extra C-terminal amino acids. Soluble neuropilins are capable of binding to VEGF165 or any form of VEGF that contains exon 7 and are useful for inhibiting VEGF interaction not only with neuropilins but also with KDR/Fik-1 and Fitl. They may also not contains the contains that contains the contains 
                                                                                                                                                           act as dominant negative receptors when expressed in cells by dimerizing with intact neuropilins are useful for tractors. The soluble neuropilins are useful for tractors.
                                          Sequence
                                                                                        tumors can
                                                                                                             associated with VEGF, e.g. metastasis, inappropriate angiogenesis, chronic inflammation, diabetic retinopathy and arthritis. Solid
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soluble human neuropilins and related polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gagnon
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09-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuropilin 2; human; vascular endothelial growth factor receptor;
VEGF165R; inhibitor; metastasis; angiogenesis; inflammation;
arthritis; diabetic retinopathy; cytostatic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY06320 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        klevstngedwmvyrhgknh--kvfqanndatevvlnklhaplltrfvrirpqtwhsgia 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VMNFKNNNSKWKTYKGIVNNEEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIA 451
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                                                                                        also be treated
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97US-0069155.
97US-0069687.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      98pp; English
                                                                                                          retinopathy and
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RESULT 12
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ID AAW962
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               Claim 1; Page 84-86; 105pp; English
                                                                                                                                                                   N-PSDB; AAX09003
                                                                                                                                                                                          WPI; 1999-120780/10
                                                                                                                                                                                                                                                     Chen H,
                                                                                                                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                     24-SEP-1997;
08-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Semaphorin receptor; SR; regulation; cell function; cell morphology; nerve cell, neuron; axon; diagnosis; therapy; detection; mutant allele; neuropilin.
                                                                  New semaphorin receptor (SR) class 1 and class 2 proteins for, e.g. regulating nerve cell function and morphology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAY-1999 (first entry)
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                                                                                                                                                                                                                                                     He Z,
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2; Mismatches 166;
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맑 S 밁 õ 밁 õ 밁 õ

Human semaphorin receptor SR2a(0) 17

12-MAY-1999 AAW96255;

(first entry)

Semaphorin receptor; SR; regulation; cell function; cell morphology; nerve cell; neuron; axon; diagnosis; therapy;

detection; mutant allele; neuropilin

W09902556-A1

Homo sapiens

RESULT 13 AAW96255

AAW96255 standard; Protein; 926

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밁 Ş 문 õ 뭐 Š

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CC Semaphorin receptor (SR) proteins are involved in nerve cell cylidance. The SR proteins can regulate cell function and morphology, especially nerve cells. Inhibitors of SR proteins promote nerve cell cyrowth. Binding agents specific to the SR polypeptides are useful CC for diagnosis and therapy, especially where disease or disease. C prognosis is associated with improper or undestrable axon outgrowth cc translation. The SR nuclei, sequences are used to provide c translatable transcripts, hybridisation probes, PCR primers, CC diagnostic nucleic acids, etc. They are used in detecting the presence of SR genes, and to identify wild type and mutant alleles. Within alleles are used to generate allele-specific oligonucleotide within talleles are used to generate allele-specific oligonucleotide composes for clinical diagnosis. The methods are used to identify gapits which modulate the activity of SR polypeptides. This sequence encodes the mouse SRZ(b) (D plypeptide which is an isoform of neuropilin-2b with 0 amino acids inserted.
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Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                     452 LKVELIGCQIT 462
                                                                 362 klevstngedwmvyrhgknh--kvfqanndatevvlnklhaplltrfvrirpqtwhsgia 419
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lrlelfgcrvt 430
                                                                                                       VMNFKNNNSKWKTYKGIVNNEEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIA
                                                                                                                                          pqqsrlhgddngwtpnldsn----keylqvdlrfltmltaiatggaisretqngyyvksy
                                                                                                                                                                                  PGQARLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTIG--STQSNFNFYVKSF
                                                                                                                                                                                                                                                        ILANGVLSRDGSLSDKRFLFTSNGCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWS
                                                                                                                                                                                                                                                                                            dckydwldiwdgiphvgpligkycgtktpselrsstgilsltfhtdmavak-----dg
                                                                                                                                                                                                                                                                                                                                                                  edcsknftspngtiespgfpekyphnldctftilakpkmeiilqflifdlehdplqvgeg
                                                                                                                                                                                                                                                                                                                                                                                                                                         ieirdgdsesadllgkhcgni-apptiissgsmlyikftsdyarggagfslryeifktgs 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cggrlnskdagyitspgypqdypshqncewivyapepngkivlnfnphfeiekhdckydf 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGHLVTYQDSGTMTSKNYPGTYPNHTVCEKTITVPK-GKRLILRLG-DLDIESQTCASDY 145
                                                                                                                                                                                                                     fsaryylvhqeplenfq-----cnvplgmesgrianeqisassty-----sdgrwt
                                                                                                                                                                                                                                                                                                                                 -CPAGCRDVAGDIS--GNMVDGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRYEG
                                                                                                                                                                                                                                                                                                                                                                                                          909 AA;
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Pred. No. 6e-22;
""" omatches 166; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 109
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08-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1999-120780/10
                                   klevstngedwmvyrhgknh--kvfganndatevvlnklhaplltrfvrirpqtwhsgia
                                                               VMNFKNNNSKWKTYKGIVNNEEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIA
                                                                                                                    PGQARLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTTG--STQSNFNFYVKSF
                                                                                                                                                fsaryylvhqeplenfq-----cnvplgmesgrianeqisassty-----sdgrwt
                                                                                                                                                                                                     dckydwldiwdgiphvgpligkycgtktpselrsstgilsltfhtdmavak-----
                                                                                                                                                                                                                                                           edcsknftspngtlespgfpekyphnldctftilakpkmeillqflifdlehdplqvgeg
                                                                                                                                                                                                                                                                                                                  ieirdgdsesadllgkhcgni-apptiissgsmlyikftsdyarggagfslryeifktgs
                                                                                                                                                                                                                                                                                                                                            LLF----TSSSDQYGPYCGSMTVPKELLLNTSEVTVRFESGSHISGRGFLLTY-----AS 196
                                                                                                                                                                                                                                                                                                                                                                     cggrlnskdagyitspgypqdypshqncewivyapepnqkivlnfnphfeiekhdckydf.87
                                                                                                                                                                                                                                                                                                                                                                                                   CGHLVTYQDSGTMTSKNYPGTYPNHTVCEKTITVPK-GKRLILRIG-DLDIESQTCASDY 145
                                                                                        pqqsrlhgddngwtpnldsn-
                                                                                                                                                                            ILANGVLSRDGSLSDKRFLFTSNGCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWS
                                                                                                                                                                                                                                 -CPAGCRDVAGDIS--GNMVDGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRYEG
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                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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97US-0889458
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                                                                                                                                                                                                                                                                                        -HPDLITC----LERASHYLKTEYSKF------
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 349; DB 20;
Pred. No. 6.2e-22;
                                                                                            keylqvdlrfltmltaiatqgaisretqngyyvksy
                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 166;
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AAY06318
ID AAY0
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         receptor of vascular endothelial growth factor (VEGP) Expression of neuropilin is associated with anglogenesis and motile metastatic cancer cells, and thus is an important target for antiangiogenic and anticancer therapy. Neuropilin-2 colk (see AAX5912) was obtained from MDA-MB-231 cells by expression cloning soluble neuropilin (see ANX60320) comprising anino acids 277-593 of the present sequence is claimed, and can be isolated from neuropilin producing cells or is recombinantly engineered from neuropilin encoding by. Soluble truncated neuropilins are capable of binding to VEGF165 or any form of VEGF that contains sxo. 7 and are binding to VEGF165 or any form of VEGF that contains sxo. 7 and are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuropilin-2; human; vascular endothelial growth factor receptor; VRGF; inhibitor; metastasis; angiogenesis; infilammation; arthritis diabetic retinopathy; cytostatic; antinflammatory; antiangiogenic; antidiabetic; ophthalmological; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human
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                                                                                                                                                    The present sequence represents human neuropilin-2, a novel
                                                                                                                                                                              Claim 4; Page 86-87;
                                                                                                                                                                                                            Soluble
                                                                                                                                                                                                                                                                              Gagnon
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09-DEC-1997;
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 therefore useful for
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Best Local Similarity 25.3
19-MAR-1998;
09-DEC-1997;
12-DEC-1997;
                                                                                                               09-DEC-1998;
                                                                                                                                                                                                                                                                                                                              antagonist; semaphori
diabetic retinopathy;
                                                                                                                                                                   17-JUN-1999
                                                                                                                                                                                                                          W09929729-A2
                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                    Human; vascular endothelial growth factor; VEGF; receptor; neuropilin; antagonist; semaphorin; collapsin; cancer; metastasis; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY14563 standard; Protein; 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neuropilins but also with KDR/FLK-1 and Fitl. The soluble NPs may also act as dominant negative receptors when expressed in cells by dimerizing with intact neuropilin receptors. The soluble neuropilins are useful for treatment of diseases or disorders associated with YBGF, e.g. metastasis, inappropriate angiogenesis, chronic inflammation, diabetic retinopathy and arthritis. Solid tumors can also be treated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          klevstngedwmvyrhgknh--kvfqanndatevvlnklhaplltrfvrirpqtwhsgia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGQARLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTTG--STQSNFNFYVKSF
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97US-0069155.
97US-0069687.
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Pred. No. 6.2e-22;
2; Mismatches 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    osteoarthritis and psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 12; 80pp; English
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420
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                              LKVELIGCQIT 462
                                                      klevstngedwmvyrhgknh--kvfqanndatevvlnklhaplltrfvrirpqtwhsgia
                                                                                  VMNFKNNNSKWKTYKGIVNNEEKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIA
1rlelfgcrvt 430
                                                                                                                                              PGQARLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTTG··STQSNFNFYVKSF
                                                                                                                                                                                                        ILANGVLSRDGSLSDKRFLFTSNGCSRSLSFE----PDGQIRASSSWQSVNESGDQVHWS
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                                                                                                                                                                                                                                                                                                                                   SD----
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                                                                                                                                                                                                                                                                                                                                                                                                                   cggrlnskdagyitspgypqdypshqncewivyapepnqkivlnfnphfeiekhdckydf 87
                                                                                                              pqqsrlhgddngwtpnldsn----keylqvdlrfltmltaiatqgaisretqngyyvksy
                                                                                                                                                                          fsaryylvhqeplenfq-----cnvplgmesgrianeqisassty-----sdgrwt
                                                                                                                                                                                                                                                                   -CPAGCRDVAGDIS--GNMVDGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRYEG
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Pred. No. 6.2e-22;
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Search completed: July Job time: 4006 sec 9 2002, 02:13:59

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seg length: 2
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Perfect score:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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     231628 seqs, 24425594 residues
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3052
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Copyright (c) 1993 - 2000
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/cgn2_6/ptodata/2/1aa/5B_COMB_pep;*
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sequence 18, Appl
sequence 22, Appl
sequence 24, Appl
sequence 34, Appl
sequence 10, Appl
sequence 11, Appl
sequence 14, Appl
sequence 14, Appl
sequence 14, Appl
sequence 24, Appl
sequence 3, Appl
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	276.5	279.5	284.5	284.5	285.5	285.5	285.5	285.5	285.5	285.5	285.5	285.5	285.5	285.5	285.5	285.5	285.5	285.5
	9.1	9.2	9.3	9.3	9.4	9.4	9.4	9.4	9.4	9.4	9.4	9.4	9.4	9.4	9.4	9.4	9.4	9.4
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ALIGNMENTS	US-09-324-867-4	US-08-162-402B-15	US-08-162-402B-5	US-07-607-538C-5	5171844-2	US-08-366-851A-2	US-08-121-202-2	PCT-US94-13200-2	PCT-US93-03275-4	US-09-324-867-3	US-09-037-601-2	US-08-670-707A-2	US-08-474-503-2	US-08-276-594A-2	US-08-212-133A-2	US-08-251-937A-4	US-07-864-004B-4	US-09-243-539-2
	Sequence 4, Appli	Sequence 15, Appl	Sequence 5, Appli	Sequence 5, Appli	Patent No. 5171844	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	-	Sequence 3, Appli	•	Sequence 2, Appli	•	•	-	Sequence 4, Appli	Sequence 4, Appli	Sequence 2, Appli

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US-08-936-135-18
                                                                           ; MOLECULE TYPE: peptide US-08-936-135-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18,
Query Match
Best Local Similarity
                                                                                                                                                                                                        TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/936,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC
                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Semaphorin Receptors NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: He, Zhigang
APPLICANT: Chen, Hang
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                                                                                                                             LENGTH: 909 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                              linear
  11.4%; 25.3%;
     Score 349; DB 3;
Pred. No. 8.6e-24;
                                                                                                                                                                                                                                                                                     UC97-288-2
                    DB 3; Length 909;
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72; Mismatches 166; Indels 84;

Gaps

16;

Matches

Conservative

16;

ON 146 LLFTSSEDOYGPYGENTUPERLINTSSTYVERESGRISGREFLIM:

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Best Local Similarity 25.3%; pred, Mo. 8.9e-24;
Matches 109; Conservative 72; Mismatches 166; Indels
                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEPAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                             FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION UNMER: 36,627
REFERENCE/DOCKET NUMBER: UC97
                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP
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APPLICANT: He, Zhigang
APPLICANT: Chen, Hang
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: HILLSBOROUGH
STATE: CALIFORNIA
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     LENGTH:
                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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901 amino acids
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Patent No. 6054293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYRE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chen, Hang
TITLE OF INVENTION: Semaphorin Receptors
NUMBER OF SEQUENCES: 26
                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346 GAISRETQKGYYVKSYKLEVSTNGEDWMVYRHGKNH--KIFQANNDATEVVLNKLHMPLL 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        378 G--STQSNFNFYVKSFVMNFKNNNSKWKTYKGIVNNEEKVFQGNSNFRDPVQNNFIPPIV 435
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                                                                               FILING DATE:
                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                         ZIP: 94010
                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                    CITY: HILLSBOROUGH
                                                                                                                                                                                                                                                                                                                    ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 CGGRPNSKDAGYITSPGYPQDYPSHQNCEWIVYAPEPNQKIVLNFNPHFEIEKHDCKYDF 87
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     REGISTRATION NUMBER:
                       NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTT 377
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OSMAN, RICHARD A FRATION NUMBER: 36,627
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                                                                                                                                                                                                                   APPLICANT: He, Zhigan
APPLICANT: Chen, Hang
TITLE OF INVENTION: S
NUMBER OF SEQUENCES:
                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           404 TRFIRIRPQTWHLGIALRLELFGCRVTDAPCSNMLGMLSGLIADTQISASSTREYLWSP
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OPERATING SYSTEM:
SOFTWARE: Patentl
                                                                                                         COUNTRY:
                                                                                                                             STATE:
                                                                                                                                                CITY: HILLSBOROUGH
                                                                                                                                                               ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE
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                               IBM PC compatible
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PatentIn Release #1.0,
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340: 24:
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                 PC-DOS/MS-DOS
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                                                                                                                                                                                                                                       Semaphorin Receptors
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  Version #1.30
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US-08-936-135-10

; Sequence 10, Application US/08936135

; Patent No. 6054293
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TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                      APPLICANT: Tessier-La
APPLICANT: He, Zhigan
APPLICANT: Chen, Hang
                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                    TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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LENGTH: 909 amino acids
TYPE: amino acid
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NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC
                                                                                                                                                                                                                                                                                                                                                                     436 ARYVRVVPQTWHQRIALKVELIGCQITQGNDSLVWRKTS---QSTSVSTKKEDETITRP 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
     CITY: HILLSBOROUGH
                                                                                                                                                                                                                                                                                                                                   404 TRFIRIRPQTWHLGIALRLELFGCRVTDAPCSNMLGMLSGLIADTQISASSTREYLWSP 462
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                                      ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 IEIRDGDSESADLLGKHCGNI-APPTIISSGSVLYIKFTSDYARQGAGFSLRYEIFKTGS 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  G--STQSNFNFYVKSFVMNFKNNNSKWKTYKGIVNNEEKVFQGNSNFRDPVQNNFIPPIV 435
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                                                                                                                                                           Tessier-Lavigne, Marc
He, Zhigang
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linear
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                                                                                                                    Semaphorin Receptors
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Pred. No. 2.8e-23;
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                                                                        Sequence 12, Application US/08936135 Patent No. 6054293
                                    GENERAL INFORMATION:
APPLICANT: Tessie
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 909 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: UC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
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                                                                                                                                                                                            404
                                                                                                                                                                                                                    436 ARYVRVVPQTWHQRIALKVELIGCQITQGNDSLVWRKTS---QSTSVSTKKEDETITRP 491
                                                                                                                                                                                                                                                                                                         378 G--STQSNENEYYKSEVMNEKNNNSKWKTYKGIVNNEEKVFQGNSNFRDPVQNNFIPPIV
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TOPOLOGY: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 CGGRPNSKDAGYITSPGYPQDYPSHQNCEWIVYAPEPNQKIVLNFNPHFEIEKHDCKYDF 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/936,135 FILING DATE:
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                                                                                                                                                                                       TRFIRIRPQTWHLGIALRLELFGCRVTDAPCSNMLGMLSGLIADTQISASSTREYLWSP 462
                                                                                                                                                                                                                                                                                                                                                                                         SSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -CPAGCRDVAGDIS--GNMVDGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRY-- 275
                                                                                                                                                                                                                                                                                                                                                                                                                              IHQEPPENFQCNVPLGMESGRIANEQISASSTFSDGR----------
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He, Zhigang
Chen, Hang
                                    Tessier-Lavigne,
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23.2%; Pred. No. 2.8
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 914 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Ser
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                  404 TRFIRIRPQTWHLGIALRLELFGCRVTDAPCSNMLGMLSGLIADTQISASSTREYLWSP 462
                                                                                                                                                                                                 304 -----wTPQQSRLHGDDNGWTPNLDSN----KEYLQVDLRFLTMLTAIATQ 345
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 CGHLVTYQDSGTMTSKNYPGTYPNHTVCEKTITVPK-GKRLILRLG-DLDIESQTCASDY 145
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                                                                                                                                                            G--STQSNFNFYVKSFVMNFKNNNSKWKTYKGIVNNEEKVFQGNSNFRDPVQNNFIPPIV 435
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                                                                                                                           GAISRETQKGYYVKSYKLEVSTNGEDWMVYRHGKNH--KIFQANNDATEVVLNKLHMPLL
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SYSTEM: PC-DOS/MS-DOS
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Pred, No. 2.9e-23;
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APPLICANT: Tessie
APPLICANT: He, Zh
APPLICANT: Chen, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 14
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ATTORREY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy
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MOLECULE TYPE:
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NUMBER OF SEQUENCES:
                                 378 G--STQSNENFYVKSFVMNFKNNNSKWKTYKGIVNNEEKVFQGNSNFRDPVQNNFIPPIV 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 CGHLYTYQDSGTMTSKNYPGTYPNHTYCEKTITYPK-GKRLILRLG-DLDIESQTCASDY 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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GAISRETQKGYYVKSYKLEVSTNGEDWMVYRHGKNH--KIFQANNDATEVVLNKLHMPLL
                                                                        -----WTPQQSRLHGDDNGWTPNLDSN----KEYLQVDLRFLTMLTAIATQ
                                                                                                       SSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSNNHKPREWLEIDLGEKKKITGIRTT 377
                                                                                                                                                                                                                  DCKYDWLDIWDGIPHVGPLIGKYCGTKTPSKLRSSTGILSLTFHTDMAVAKDGFSARYYL
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                                                                                                                                                                                                                                                                                                                            SD---
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                                                                                                                                                                                                                                                                                                                                                                                                                                 CGGRPNSKDAGYITSPGYPQDYPSHQNCEWIYYAPEPNQKIVLNFNPHFEIEKHDCKYDF 87
                                                                                                                                              IHQEPPENFQCNVPLGMESGRIANEQISASSTFSDGR-----
                                                                                                                                                                                                                                                      -CPAGCRDVAGDIS--GNMVDGYRDTSLLCKAAIHAGIIADELGGQISVLQRKGISRY--
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75 DENISE DRIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   He, Zhigang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version
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                                                                                                                                                                                -----EGILANGVLSRDGSLSDKRFLFTSNGCSRSLSFEPDGQIRAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.3%; Score 343.5;
23.2%; Pred. No. 2.9
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US-08-936-135-16
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INFORMATION FOR SEQ ID NO:
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TOPOLOGY: 11:
MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
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NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Semaphorin Receptors NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: He, Zhigang
APPLICANT: Chen, Hang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                 147
                  267 IHQEPPENFQCNVPLGMESGRIANEQISASSTFSDGR-----
                                                                                                                                                                                          146 LLF----TSSSDQYGPYCGSMTVPKELLLNTSEVTVRFESGSHISGRGFLLTY-----AS 196
                                                                                                                                                                                                                             88 IEIRDGDSESADLLGKHCGNI-APPTIISSGSVLYIKFTSDYARQGAGFSLRYEIFKTGS 146
                                                                                                                                                                                                                                                                                                                                                                         Local Similarity hes 111; Conserv
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                                                                                                                                                                                                                                                                                               28 CGGRPNSKDAGYITSPGYPQDYPSHQNCEWIVYAPEPNQKIVLNENPHFEIEKHDCKYDF 87
                                                                                                                                                                                                                                                                                                                               88 CGHLVTYQDSGTMTSKNYPGTYPNHTVCEKTITVPK-GKRLILRLG-DLDIESQTCASDY 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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FILING DATE:
CLASSIFICATION: 435
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
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                                                                                      DCKYDWLDIWDGIPHVGPLIGKYCGTKTPSKLRSSTGILSLTFHTDMAVAKDGFSARYYL 266
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550) 343-4342
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23.2%; Pred. No. 3e
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                                                                                                                                                                                                                                              Matches 113;
                                                                                                                                                                                                                                                                            Query Match
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                                116 GPFLFIKFVSDYETHGAGFSIRYEIFKRGPECSQNYTAPTGVIKSPGFPEKYPNCLECTY 175
                                                                                                                                     118 TITVPKG-KRLILRLG-DLDIESQTCASDYLLFTSSSDQ----YGPYCGSMTVPKELLLN 171
                                                                 172 TSEVTVRFESGSHISGRGFLLTYA----------SSDHPDLITC-- 205
                                                                                                    57 LIQAPEPYQRIIINFNPHFDLEDRDCKYDYVEVIDGENEGGRLWGKFCGKI-APSPVVSS 115
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-936-135-6
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Patent No. 6054293
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INFORMATION FOR SEQ ID NO:
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ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
NA
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APPLICATION NUMBER: US
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APPLICANT:
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                                                                                       64 RGL-----LALLLAVSAPLRLQAEELGDGCGHLVTYQDSGTMTSKNYPGTYPNHTVCEK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              404 TRFIRIRPQTWHLGIALRLELFGCRVTDAPCSNMLGMLSGLIADTQISASSTREYLWSP 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            436 ARYVRVVPQTWHQRIALKVELIGCQITQGNDSLVWRKTS---QSTSVSTKKEDETITRP 491
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                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: CALIFORNIA
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RGLPLLCATLALALAGAFR-----SDKCGGTIKIENPGYLTSPGYPHSYHPSEKCEW 56
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amino acid
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He, Zhigang
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550) 343-4342
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                                                                                                                                                                                                                                       Score 329; DB 3;
Pred. No. 6.8e-22;
                                                                                                                                                                                           Mismatches 161;
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US-07-607-538C-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS 5.0

SOFTWARE: PatentIn Re-lease #1.0, Version #1.25

CURRENT APPLICATION DATA:
                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 943-1931
                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel
REGISTRATION NUMBER: 30,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                  FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     377 KAIIFQGNTNPTDVVLGVFSKPLITRFVRIKPVSWETGISMRFEVYGCKIT 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 TSNGCSRSLSFEP----DGQIRASSSWQSVNESGDQVHWSPGQARLQDQGPSWASGDSSN 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 IIFAPKMSEIILEFESFDLEQDSNP--PGGMFCRYDRLEI----WDGFPE-----VGPH
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/607,538C FILING DATE: 01-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                         TOPOLOGY:
                                                                                           TYPE: amino acid
                                                                                                                                                                         TELEX: N.A.
                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                           STRANDEDNESS:
                                                                                                                LENGTH:
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T: 2055 No. 5455031th Broadway
Walnut Creek
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                                                                                                                218 amino acids
                                                                                                                                                                                            (510) 943-1189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Larocca, David J.
                                                         linear
                                    protein
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DIFFERENTIATION ANTIGEN BINDING SPECIFITY AND CLOTTING
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Query Match Best Local Similarity

10.5%;

Score 321; DB 1; Pred. No. 3.5e-22;

Length 218;

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353 NNHKPREWLEIDLGEKKKITGIRTTGSTQSNFNFYVKSFVMNFKNNNSKWKTYKGIVNNE 412

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58 NGCSTPLGMENGKIENKQITASSFKKSWW-----GD--YWEPFRARLNAQGRVNAWQAKA 110

300 NGCSRSLSFE----PDGQIRASS---SWQSVNESGDQVHWSPGQARLQDQGPSWASGDSS 352

16;

Gaps

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Matches

Conservative

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; STRANDEDNESS:
; TOPOLOGY: unk.
; MOLECULE TYPE: |
US-08-162-402B-4
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              Query Match
Best Local Similarity
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                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: P6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: 46 KDALTON HUMAN MILK FATITLE OF INVENTION: GLOBULE (HMFG) ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: PETERSON, JEKKI A
APPLICANT: LAROCCA, DAVID J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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CITY: Los Angeles
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                                                                                                                                                                 TYPE:
                                                                                                                                                                                                                                           TELEX
                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 30,930
                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
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                                                                                                                                                                                                                                                          TELEFAX: 213-489-4210
                                                                                                                                                                                                                                                                                                                                                      NAME: Amzel, Viviana
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                  LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CERIANI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FastSEQ for Windows Version
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                                                                                                                                                                                  amino acids
                                                                                                     peptide
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N: 435
                                                                                                                                                  unknown
10.5%; Score 321; DB 2; I
42.6%; Pred. No. 3.5e-22;
42.6%; Mismatches 51;
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                                     Length 218;
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RESULT 14
US-08-162-402B-14
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                                                     Sequence 14, Application US/08162402B Patent No. 5972337
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                    GENERAL INFORMATION:
APPLICANT: CERIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
  APPLICANT:
                                                                                                                                                                 2134 DKIFEGNSNTKGHMKNFFNPPIISRFIRIIPKTWNQSIALRLELFGCDI 2182
                                                                                                                                                                                                                                      2076 NNNK--QWLQVDLLKIKKVTAIVTQGCKSLSSEMYVKSYSIQYSDQGVANKPYRQKSSMV 2133
                                                                                                                                                                                                                                                                                                                  2023 NGCSTPLGLEDGRIQDKQITASSFKKSWW-----GD--YWEPSLARLNAQGRVNAWQAKA 2075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Compositions And Methods For Screening: TITLE OF INVENTION: Compounds For Anticoagulant Activity NUMBER OF SEQUENCES: 54
                                                                                                                                                                                                     413 EKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGCQI 461
                                                                                                                                                                                                                                                                                        353
                                                                                                                                                                                                                                                                                                                                                     300 NGCSRSLSFE----PDGQIRASS---SWQSVNESGDQVHWSPGQARLQDQGPSWASGDSS 352
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APPLICANT: Cui,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   413 EKVFQGNSNFRDPVQNNFIPPIVARYVRVVPQTWHQRIALKVELIGCQI 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2183 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                    Match 10.48;
Local Similarity 40.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ingolia, Diane E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 06-NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                            NNHKPREWLEIDLGEKKKITGIRTTGSTOSNFNFYVKSFVMNFKNNNSKWKTYKGIVNNE 412
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PETERSON, JERRY A.
                 CERIANI, ROBERTO L
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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(415) 397-8338
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Pred. No. 3.1e-20;
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; GENERAL INFORMATION:
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                                                                                                                                                                                                                                         Sequence 2, Application US/09324867F Patent No. 6251632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 10.2%;
Best Local Similarity 41.7%;
Matches 70; Conservative 3
TITLE OF INVENTION: CANADE FACTOR VIII Gene, FILE REFERENCE: 1659.0010002/JAG/BBU CURRENT APPLICATION NUMBER: US/09/324,867A CURRENT FILING DATE: 1999-06-03 CHARLER APPLICATION NUMBER: 09/035,141
                                                                                                                        APPLICANT: Lillicrap, David
APPLICANT: cameron, Cherie
APPLICANT: No. 6251632Ley, Colleen
APPLICANT: Horrocks, L. Suzanne Ho
                                                                                                          APPLICANT: Hough, Christine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: 4
TITLE OF INVENTION: G
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                            112 KIFEGNTNTKGHVKNFFNPPIISRFIRVIPKTWNQSITLRLELFGCDI 159
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STRANDEDNESS:
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STREET: 444 South Flower St., 19th Floor
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Pred. No. 1.8e-21;
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                                                                                       Protein and Methods of Use
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Sequence: Title

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Novel nucleic acid encoding human CUB-domain containing protein, useful for drug screening, diagnosis and treatment of physiological disorders WPI; 2001-290917/30. Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B, Sands AT;

Claim 1; Page 27; 33pp; English.

or diseases -

The sequence represents a polynucleotide which encodes a novel human protein (NHP) containing a CUB domain (an extracellular domain). CUB proteins have been associated with regulating development, modulating cellular processes and preventing infectious disease. NHP nucleotide sequences are useful for gene therapy of physiological disorders or consening libraries and assessing gene patterns. NHP pulceotide sequences care useful for detecting mutant or inappropriately expressed NHPs (for cerample, those proteins associated with obesity, high blood pressure, connective tissue disorders and intertility) for the diagnosis of a disease. The polynucleotides may also be used in screening for drugs effective in the treatment of symptomatic or phenotypic manifestations of concentrate in the normal function of NHP in the body. Nucleotide constructs care speciation of compounds that bind to NHP receptors or trigger culentification of compounds that bind to NHP receptors or trigger culentification of compounds that bind to NHP receptors or trigger

Sequence 1761 BP; 471 A; 402 C; 483 G; 405 T; 0 other;

Obery Match Best Local Similarity 100.0%; Score 1761; DB 22: Length 1761; Best Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0; Matches 1761; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Indels 0;

у	Db	Qy	Qу Db	Db	Qy	Db	Qy	DЪ	Qy	₽	Qy	DЪ	Qy	몽	νQ	₽	Qy	Вb	Qy	Db ·	Qy	Db	Qy	рь	Qy	밁	Qy	Db	Οу	DЪ	Qy	DЬ	Qy	DЬ
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gaggeteagaaaacagaetgttggaageagattaaatatecetttgecagaeateagtea 1	tggggatctttgcagcctt	tggggatctttgcagcctttagaaagaagaagaagaagaaggaag	ataaacattacaacggfggctatrccattggtgctccttgttgtcctgggtggttggga	ctaagaagaagatgagacaatcacaaggcccatcccctcggaagaaacat	aagaaagaagatgagacaatcacaaggcccatcccctcggaagaaacatccacagg	gat	ttacacaaggtaatgattcattggtgtgtggcgcaagacaagtcaaagcaccagtgtt	tgg	ttgtcccccagacatggcaccagaggatagccttgaaggtggagctcattggttgc	aactttogggacccagtgcaaaacaatttcatccctcccatcgtggccagatatgtgcgg	acttrogggacccagtgcaaaacaatttcatccctcccatcgtggccagatatgtgcg	aagtggaagacctataaaggaattgtgaataatgaagaaaaggtgtttcagggtaactct	agtggaagacctataaaggaattgtgaataatgaagaaaaggtgtttcagggtaactc	caactttatgttaagagttttgtgatgaacttcaaaaacaataattct	agtcgaacttcaaacttttatgttaagagttttgtgatgaacttcaaaaaacaataattc	tttgggggagaaaaagaaataacaggaattaggaccacagg	tggagatcgatttgggggagaaaaagaaaataacaggaattaggaccacaggatctaca	gaccaaggcccatcatggcttcgggcgacagtagcaacaaccaccaccaacca	accaaggcccatcatgggcttcgggcgacagtagcaaccaccacaaaccacgagagtg		agtoggtoaatgagagtggagaccaagttoactggtotoctggccaagcccgacttoa	ggttgcagcagatcottgagttttgaacctgacgggcaaatcagagcttcttcctcatgg	gttgcagcagatccttgagttttgaacctgacgggcaaatcagagcttcttcctcatgg	aatggtgttctttcgagggatggttccctgtcagacaagcgatttctgtttacctccaat	alggtgttctttcgagggalggttccctgtcagacaagcgalttctgtttacctccaat		gtggccagatcagtgtgcttcagcgcaaagggatcagtcgatatgaagggattctggcc	agagatacctctttattgtgcaaagctgccatccatgcaggaataattgctgatgaacta	gagatacctctttattgtgcaaagctgccatccatgcaggaataattgctgatgaact	tgcccagctggttgtagagacgtagcaggagacatttctgggaatatggtagatggatat	gcccayctggttgtagagacgtagcaggagacatttctgggaatatggtagatggata	gatttaataacatgtttggaacgagctagccattatttgaagacagaatacagcaaattc	atttaataacatgtttggaacgagctagccattatttgaagacagaatacagcaaatt	
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Datebase: N_ genesey-032802
AC NO! AASOOGO
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anaphylaxis, hepatitis, multiple sclerosis, cancer, coronary artery disease, malaria, atopic dermatuts, amyotrophic lateral sclerosis, meningitis, attention deficit disorder, Crohn's disease, gastroenteriti goltre, hypoglycamia, disbetes mallitus, endometricasis, pulmonary embolism and muscular dystrophy, Antibodies to disorders such as these can be made by providing a polypeptide of the invention to an immuno-competent vertebrate and harvesting blood or serum from the

gastroenteritis,

vertebrate.

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acaagtgatatggcaggttaa 1761
                                              gctgagtttaccatcagctatgataatgagaaggagatgacacaaaagttagatctcatc 1740
           acaagtgatatggcaggttaa 1761
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07-SEP-2001 AAS00660 standard; N (first entry) CDNA; 3594 먪

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Human TANGO 229 cDNA

Human; TANGO 229; T cell; heart; liver; pancreas; placenta; brain; lung;

skeletal muscle, kidney, spleen; lymph node; peripheral blood leukocyte; bone marrow; thymus tissue; abnormal blood congulation; asthma; cancer; anaphylaxis; hepatitis; multiple scierosis; coronary artory disease; ss; analaria; atopic dermatitis; amyotrophic lateral scierosis; meningitis; attention deficit disorder; Crohn's disease; gastroenteritis; optice; hypodycaemia; diabetes mellitus; endometriosis; pulmonary embolism; hypodycaemia; diabetes mellitus; endometriosis; pulmonary embolism; dystrophy; immuno-competence; vertebrate; blood; serum.

Homo sapiens

_19-OCT-1999; 23-JUN-2000; 26-APR-200 mat_peptide 2000WO-US17386 99US-0420707 /*tag= b 174..2216 /product-72 173 /product-/*tag-Location/Qualifiers 72..2219 /*tagа "Mature "Human TANGO human TANGO

(MILL-) MILLENNIUM PHARM

Mackay CR, Myers PS, Kirst SJ, Fraser CC, Leiby · KR

2001-308477/32 AAU00670

regulating cellular processes New isolated nucleic acid molecule for diagnosis, therapy of human and other animal disorder, or as prevention, and modulating agen agent

Claim 1; Fig 1; 263pp; English.

The sequence represents a cDNA which encodes human TANGO 229 polypeptide. This protein and similar others exhibit the ability to affect growth, proliferation, survival, differentiation, activity, morphology, or movement/majoration of, e.g. T cells and cells of the heart, liver, pancreas, placenta, brain, lung, skeletal muscle, kidney, spleen, lymph node, peripheral blood leukocyte, bone marrow or thymus tissue. They can be used as modulating agents for regulating cellular processes, thus, the proteins and their associated nucleic acids can be used to prognosticate, prevent, diagnose, or treat disorders associated with physiological prevent, diagnose, or treat disorders associated with physiological disorders include abnormal blood coagulation,

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Query Match 95.8%;
Best Local Similarity 99.9%;
Matches 1688; Conservative
                                            Sequence 3594 BP;
                                            958 A;
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Score 1686.8;
Pred. No. 0;
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601 671 541 611 gttgtagagacgtagcaggagacatttctgggaatatggtagatggatatagagatacct gttgtagagacgtagcaggagacatttctgggaatatggtagatggatatagagatacct catgtttggaacgagctagccattatttgaagacagaatacagcaaattctgcccagctg catgtttggaacgagctagccattatttgaagacagaatacagcaaattctgcccagctg

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Best Local Similarity
Matches 1620; Conserv
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18-FEB-2000;
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ty; high blood pressure;
ediated pathway; ds.
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connective tissue disorder; infertility;
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The sequence represents a polynuclotide which encodes a novel human protein (NHP) containing a CUB domain (an extracellular domain). CUB protein have been associated with regulating development, modulating cellular processes and preventing infectious disease. NHP nucleotide sequences are useful for gene therapy of physiological disorders or diseases. NHP oligonucleotides are useful as hybridisation probes for screening librories and assessing gene patterns. NHP nucleotide sequences are useful for detecting mutant or inappropriately expressed NHPs (for example, those proteins associated with obesity high blood pressure, connective tissue disorders and infertility) for the diagnosis of a disease. The polynucleotides may also be used in screening for drugs effective in the treatment of symptomatic or phenotypic manifestations of

Disclosure; Page 30-31;

33pp; English

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                              perturbing the normal function of NHP in the body. Nucleotide constructs encoding NHP products are used to genetically engineer host cells to express such products in vivo. These host cells allow for the identification of compounds that bind to NHP receptors or trigger NHP mediated pathways.
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Sequence 1768 BP; 539 Ą. 370 Ç 421 . G 438 Ŧ, 0 other.

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gacatotaagaattatocogggacotacocodatoacaotgtttgcgaaaagacaattac
                         ggcggaggagctgggtgatggctgtggacacctagtgacttatcaggatagtggcacaat
                                                                        Similarity
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100.0%;
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밁 õ 밁 360 61 agtaccaaaggggaaaagactgattctgaggttgggagatttggatatcgaatcccagac gacatctaagaattatcccgggacctaccccaatcacactgtttgcgaaaagacaattac

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무양 301 540 gagtggatcccacatttctggccggggttttttgctgacctatgcgagcagcgaccatcc gagtggatcccacatttctggccggggttttttgctgacctatgcgagcagcgaccatcc 360 599

Ş B 8 DЬ 361 600 agatttaataacatgtttggaacgagctagccattatttgaagacagaatacagcaaatt agatttaataacatgtttggaacgagctagccattatttgaagacagaatacagcaaatt 420 659

밁 9 421 660 ctgcccagctggttgtagagacgtagcaggagacatttctgggaatatggtagatggata ctgcccagctggttgtagagacgtagcaggagacatttctgggaatatggtagatggata 480

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유 원 문 õ 840 601 541 caatggtgttctttcgagggatggttccctgtcagacaagcgatttctgtttacctccaa caatggtgttctttcgagggatggttccctgtcagacaagcgatttctgttttacctccaa aggtggccagatcagtgtgcttcagcgcaaagggatcagtcgatatgaagggattctggc aggtggccagatcagtgttgcttcagcgcaaagggatcagtcggttgtagagggattctggc 600 839

문 Q 문 õ 960 900 gcagtcggtcaatgagagtggagaccaagttcactggtctcctggccaagcccgacttca gcagtcggtcaatgagagtggagaccaagttcactggtctcctggccaagcccgacttca tggttgcagcagatccttgagttttgaacctgacgggcaaatcagagcttcttcctcatg tggttgcagcagatccttgagttttgaacctgacgggcaaatcagagcttcttcctcatg 780 1019 720

õ 밁 9 밁 841 781 gctggagatcgatttgggggagaaaaagaaaataacaggaattaggaccacaggatctac gctggagatcgatttgggggagaaaaaggaaataacaggaattaggaccacaggatctac ggaccaaggcccatcatgggcttcgggcgacagtagcaacaaccacaaaccacgagagtg ggaccaaggcccatcatgggcttcgggcgacagtagcaacaaccacaaaccacgagagtg 1079 840

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RESULT AAA96736 ID AAAS AAA96736 G standard;

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cacaagtgatatggcaggttaa

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DNA;

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(first

entry)

19-FEB-2001

Polynucleotide isolated from lymph node stromal cells of. fsn ; mice

immune system oblood vessel grainflammatory bo cardiac node stromal cell; fsn -/- mice; inflammatory disorder; e system disorder; cancer; viral disorder; HV infection; l vessel growth; tumour necrosis factor disorder; arthritis; encorary bowal disease; fibroblast growth factor-mediated disorder; failure;

Mus

CDS Location/Qualifiers 64..1575 /*tag= a

WO200058463-A1

05-OCT-2000

18-FEB-2000; 2000WO-NZ00015

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a polynucleotide sequence which is isolated from lymph node stromal cells of fsn -/- mice. The polynucleotides and their polypepides are useful for treating an inflammatory disorder, disorder of immune system and cancer selected from epithelial, lymphold, myelold, stromal and neuronal cancers, a viral disorder, in particular HIV infection and for modulating the growth of blood vessels. The polypepides are useful for treating a tumour necrosis factor (TNV) mediated disorder, such as those selected from arthritis, inflammatory bowel disease and cardiac failure and a fibroblast growth factor-mediated disorder. It is also useful in assays to determine biological activity, to raise antibodies, to isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polypeptide expressed in mammalian fan '- lymph node stromal cells, useful for modulating growth of blood cells, for treating inflammatory and tumour necrosis factor mediated disorders, cancer and viral
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P-PSDB; AAB19126.
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the proteins are collectively known as colon cancer antigens, the colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectlying mutations or deletions in a pattent's genome that affect the activity of P by expressing inactive proteins or to supplement the pattents own production of P. Additionally, N may be used to produce the oclon cancer associated Ps. by inserting the nucleic acids into a host cell and culturing the call to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AMH37196 to AMH37204
                                                                                                                                                                       AAH32943 to AAH37195 and AAG73514 to AAG777788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where
                                                                                                                                                                                                                                       Claim 1;
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03-NOV-1999;
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P-PSDB; AAG75450.
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and/or treating colorectal cancers -
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N.B. Pages 666 to 682 and page 7053 of the missing at time of publication, meaning no SEQ ID NO:1027 to 1052, 7921 and 7922.
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                         This sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources: The EST sequences and proteins encoded by them are predicted to have useful bloogical activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopolesis regulating activity, tissue growth activity, haematopolesis regulating activity, the supporting data is given activity, the activity, haematopolesis regulating activity, the providence for activity, anti-inflammatory activity, catherinthumour invasion suppressor activity, anti-inflammatory activity, adherinthumour invasion suppressor activity, anti-inflammatory activity, adherinthumour invasion suppressor activity.
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The present sequence is a cDNA encoding human Factor 8 homologue (F8H) which is a coagulation cofactor. The protein is selectively expressed in haematopoletic, heart and reproductive tissues. It has haemastatic and cerebroprotective activities. The F8H contains a Factor 5/8 signature and is useful as a therapeutic for treating coagulation related diseases such as haemophilia and stroke. The nucleic acid is useful as hybridisation probe and amplification primer for detecting deficiencies
                                                                                                                                                                                                                                                                                                                                                                                                                                           04-JUL-2000
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                                                                          in the level of F8H mRNA, for screening F8H gene mutations and for monitoring regulation of gene expression. Fragments of the nucleic aci are also useful as diagnostic probes and primers, and can be used in screening methods such as those using DNA chips. The present sequence also useful as a target to screen therapeutically useful modulators
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Sequence 2046 BP; 615 A; 457 ç 467 <u>ن</u> 507 H 0

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RESULT AAH36736

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03-SEP-2001 AAH36736;

Human colon

Databere: N-Genesey-Ac NO: AA X 32182 032802

Page

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Query Match
Best Local Similarity
Matches 189; Conserv cancer associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in generic therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with happropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer associated Ps. by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and AAR77789 represent sequences used in the exemplification of the recent invariance. 1206 gaagacctataaaggaattgtgaataa-tgaagaaaaggtgtttcagggtaactctaact 1264 N.B. Pages 666 to 682 and page 7053 of the sequence missing at time of publication, meaning no sequences SEQ ID NO:1027 to 1052, 7921 and 7922. present invention. AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers colorectal carcinoma; (HUMA-) HUMAN GENOME SCI INC 28-SEP-2000; 2000WO-US26524 Human; colon cancer; colon cancer antigen; diagnosis; detection; AAH36736 standard; cDNA; ttcgggacccagtgcaaaacaatttcatccctcccatcgtggccagatatgt-gcgggtt 1323 ttcgggacccacatgcacngcagnncatacctcccatngtggccagatatgtcgcggatt 138 gnggacctatanaggaattgtgagtaagagaataaaaggtgtntcaggggaactctaact 78 2001-235357/24. DB; AAG77329. 252 BP; 68 A; Page 5674-5675; 9803pp; English. Barash SC, Conservative cancer antigen (first entry) 99US-0157137 99US-0163280 7.2%; 81.1%; 28 56 C; 68 G; Birse 252 encoding cDNA SEQ ID NO:3818 0 CE, Pred. No. Score 127.2; ВP Mismatches 47 Rosen CA; T; 13 other 6.9e-2 DB 22; sequence listing were sequences are present for 39; Indels Length 252; 5 Gaps 4 Дb δõ 밁 RESULT AAZ32182 PN XX XX XX DE Ş ΧŞ 밁 20 ij Matches Best Query Match AM32159 to AM22144 represent reference alleles for specifically claimed nucleic acid sequences from the present invention which comprise polymorphic sites as given in a table in the specification, selected from 92 single nucleotide at the polymorphic sites as given in a table in the specification, selected to polymorphic sites as different from a nucleotide at the same site in a reference allele. The nucleic acids, and primers and probes, are used identify polymorphisms, which may predispose an individual to disease, especially a vascular disease. They can also be used in phenotype correlations, forensics, paternity testing, medicine or genetic analysis, AM4950 to AM49573 represent the proteins which correspond to some of the reference alleles. 6326 6266 aatggatgttccacaccccctgggtatggaaaatggaaagatagaaaacaagcaaatcaca 6325 Sequence 6893 BP; 2090 A; 1700 C; 1423 G; 1680 T; Claim 1; Fig 26; 134pp; English. predisposition to Determination of polymorphisms in genes, especially those identifying (WHED) WHITEHEAD INST BIOMEDICAL 26-MAR-1999; 07-OCT-1999 WO9950454-A2 Homo sapiens. polymorphic site; Human; coding sequence polymorphism; vascular pathology gene; Human coagulation factor V nucleotide sequence 13-JAN-2000 AAZ32182; 1384 acacaaggtaargattcattggtgtggcgcaa--gacaagtcaaagcaccagt 1434 1324 898 aatggttgcagcagatccttgagttttgaacctgacgggcaaatcagagcttcttcctca 957 Lander ES, medicine; genetic AAZ32182 199 139 Local Similarity 10 tggcagtcggtcaatgagagtggagaccaagttcactggtctcctggccaagcccgactt 1017 gcttcttcgtttaagaaatcttggtggggagattactgggaaacccttccgtgcccgtctg 1999-620066/53 gtcccccagacatggcaccagaggatagccttgaaggtggagctcattggttgccagatt 1383 -cacaaggtaatgattcattgngagtggtgcancganaagtcagagcaccagt gtnccncagacatggcaccaaaggatagccttgaaggaggagctcattggatgccagatt 249; AAY49563 standard; Conservative Daley (first entry) 99WO-US06473 98US-0054272 e G analysis; vascular disease; ds vascular phenotype 5.4%; cDNA; Cargill M, 6893 disease 0. correlation; forensic; paternity testing; Score 94.4; DB 20 Pred. No. 8.7e-14; ВP Mismatches RES Ireland JS, DB 20; Rozen 0 other;

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29-SEP-1999; 03-NOV-1999;

05-APR-2001 WO200122920-A2 Homo sapiens

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Sequence

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Length 6893; Indels

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The probes/primers given in ANY03921-31 are used to isolate and/or amplify and/or detect mutations in human factor-v DNA (AAT03920), esp. in DNA encoding the APC binding and/or cleavage site.
                                                                                                                     Screening for genetic defect associated with thrombosis and/or por
anticoagulant response to activated protein C useful to determine
homozygosity or heterozygosity for a mutation in Factor V, Va, VIII
   Sequence 6909
                                                                                  Claim 16; Page 60-65; 98pp; English.
                                                                                                                or VIIIa
                                                                                                                                                                                                                                                                                                                                                                                                      Factor-V; thrombosis; thrombophilia; diagnosis; anticoagulant;
activated protein-C; APC; homozygosity; heterozygosity; ss.
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Query Match Best Local Similarity

51.0%;

Score Pred.

92.8; No. 2

DB 16;

Length 6909

gene therapy protocols

New transgenic mice expressing activated protein C resistant factor V and factor V until transgenic mice useful for screening anticoagulants, as models for human thrombophilia and as models for testing in utero

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Gene polymorphism; hu
diabetes; FPCR; SSCP;
                                                     Human Vth aggregation factor protein encoding cDNA
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                                                                                                                                                                         AAZ39631 standard;
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nes 248; Conservation
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  human; Vth aggregation factor; genetic CP; fluorescence-based polymerase chain
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Pred. No. 2.3e-13;
0; Mismatches 232;
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                                                                                                                                                                                                                                            The invention provides a method for the discrimination of the gene polymorphism of human vth aggregation factor, where one of the following (1) to (6)) residues/noucleotides in the aggregation gene is discriminated in the patient to be tested :(1) residue 495: guanine (3) or adenine (A), (2) residue 642: (3) or thymine (7), (3) residue 2663: (6) or (A), (4) residue 2763: (6) or (A), (5) residue 2863: (A) or (G), (6) residue 5112: (A) or (G), The method is useful in the genetic diagnosis of a diabetes patient. The method uses FCR-SGC (fluorescence-based polymerase chain reaction-single strand conformation polymorphism) for analyzing DNA samples for polymorphisms. The present sequence represents a cDNA encoding a human vth aggregation factor protein.
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nes 248; Conserv
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Matches 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for diagnosing, prognosing or monitoring a prostate disorder. It
also provides a means of distinguishing prostate cancer from bening
prostatic hyperplasia (BBH) and for identifying potential anti-prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The patent discloses a method for diagnosing, prognosing or monitoring a prostate disorder which involves the analysis of 26 gene transcripts (referred as markers) that exhibit aberrant expression levels in prostate disorder rissues and provides a means of early diagnosis. This method is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diagnosing and monitoring prostate disorders, by analysis of 26 transcripts that exhibit aberrant expression levels in prostate disorder tissues, and provides a means of early diagnosis.
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Sequence
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RESULT 15
AAT33948
ID AAT339
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A mutant human Factor V cDNA (AAT33948) has adenine at position 1691, whereas the normal cDNA (AAT33942) has guanine at this position. The substn. results in activated protein C resistance in humans. The mutation can be detected by CR amplification of the affected region (see also AAT33935, AAT33939-41) and analysis of the products (see also AAT3394-50), either by nucleotide sequencing or by differential digestion using MnII restriction endonuclease (see also AAT33937-38).
                                                                                                                                                                                                           Claim 22; Page 146-149; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
allele
                                                                                                                                                                                                                                                          Detection of Factor V gene mutation - by PCR amplification to identify exon 10 guanine 205 or 1691 to adenine substitution, results in activated Protein C resistance
                                                                                                                                                                                                                                                                                                                                                                                                       Gandrille
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Factor V; activated Protein C resistance; APC; genetic screening;
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6754	1378	6694	1318	6634	1258	6574	1198	6514	1138	6454	1078	6400	1018	6340	958	6280	898	Query Match Best Local Matches 24
gatatt 6759	cagatt 1383	cgtgtcattcctaaaacatggaatcaaagtattacacttcgcctggaactctttggctgt 6753	cgggttgtcccccagacatggcaccagaggatagccttgaaggtggagctcattggttgc 1377	actaataccaaaggacatgtgaagaactttttcaaccccccaatcatttccaggtttatc 6693	totametttogggacccagtgcaaaacaatttcatccctcccatcgtggccagatatgtg 1317	gtggaatggaaaccatacaggctgaaatcctccatggtggacaagatttttgaaggaaat 6633	tctaagtggaagacctataaaggaattgtgaataatgaagaaaaggtgtttcagggtaac 1257	aagtetetgteetetgaaatgtatgtaaagagetataeceateeactaeagtgageaggga 6573	acacagtcgaacttcaacttttatgttaagagttttgtgatgaacttcaaaaacaataat 1197	tggctagaaattgatctactcaagatcaagaagataacggcaattataacacagggctgc 6513	tggctggagatcgatttgggggagaaaaaagaaaataacaggaattaggaccacaggatct 1137	aatgcccagggacgtgtgaatgcctggcaagccaaggcaaacaacaataagcag 6453	caggaccaaggcccatcatgggcttcgggcgacagtagcaacaaccaccacaaccacgagag 1077	gcttcttcgtttaagaaatcttggtggggagattactggggaacccttccgtgcccgtctg 6399	tggcagtcggtcaatgagagtggagaccaagttcactggtctcctggccaagcccgactt 1017	aatggatgttccacacccctgggtatggaaaatggaaagatagaaacaagcaaatcaca 6339	aatggttgcagcagatccttgagttttgaacctgacgggcaaatcagagcttcttcctca. 957	Query Match 5.3%; Score 92.8; DB 17; Length 6925; Best Local Similarity 51.0%; Pred. No. 2.3e-13; Matches 248; Conservative 0; Mismatches 232; Indels 6; Gaps 1;

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Calculated physical property data is now available. See HELP PROPERTIES for more information. See STNote 27, Searching Properties in the CAS Registry File, for complete details: http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf

=> e animal E1 E2 E3 E4 E5	cub domain protein/cn 5 1 ANIMAL BLACK/CN 1 ANIMAL BLOOD, DENATURED/CN 0> ANIMAL CUB DOMAIN PROTEIN/CN 1 ANIMAL EXTRACTS, LIVER/CN 1 ANIMAL FAT OLEINS/CN
=> e cub dor	ain/cn 5
E1	1 CUAUII/CN
E2	1 CUAUTHEMONE/CN
E3	0> CUB DOMAIN/CN
E4	1 CUB DOMAIN-CONTAINING PROTEIN 1 (HUMAN A549/CALU 6 CELL GENE
	CDCP1 PRECURSOR) /CN
E 5	1 CUB-DOMAIN-CONTAINING PROTEIN RP43 (RIFTIA PACHYPTILA)/CN
	CN CONTAINING PROTEIN RP45 (RIFTIA PACHYPTILA)/CN
=> e	
E6	1 CUB2/CN
E7	1 CUBA BLACK/CN
E8	1 CUBA ORANGE/CN
E9	1 CUBA6/CN
E10	1 CUBANA BROWN/CN
E11	1 CUBANA BROWN R/CN
E12	1 CUBANE/CN
E13	1 CUBANE RADICAL CATION/CN
E14	1 CUBANE-1,2,4,7-TETRAAMMONIUM DINITRAMIDE/CN
E15	CUBANE-1,4-DIAMMONIUM DINITRAMIDE/CN
E16	1 CUBANE-1,4-DICARBOXYLIC ACID-1,4-PHENYLENEDIAMINE COPOLYMER/
	CN
E17	1 CUBANE-1,4-DICARBOXYLIC ACID-1,4-PHENYLENEDIAMINE COPOLYMER, SRU/CN
=> s e4-5	
> 2 34-2	1 "CIB DOMAIN-COMMAINING PROMPTY 1
	1 "CUB DOMAIN-CONTAINING PROTEIN 1 (HUMAN A549/CALU 6 CELL GENE CDCP1 PRECURSOR)"/CN
	1 "CHR-DOMAIN-COMMAINING PROMPTH PRAG (
L1	1 "CUB-DOMAIN-CONTAINING PROTEIN RP43 (RIFTIA PACHYPTILA)"/CN
	2 ("CUB DOMAIN-CONTAINING PROTEIN 1 (HUMAN A549/CALU 6 CELL GENE CDCP1 PRECURSOR)"/CN OR "CUB-DOMAIN-CONTAINING PROTEIN 1

CDCP1 PRECURSOR) "/CN OR "CUB-DOMAIN-CONTAINING PROTEIN RP43

.

(RIFTIA PACHYPTILA)"/CN)

	=> e coagula E1 ' E2 E3 E4 E5	1 1	factors v/cn 5 COAGULATION FACTOR XIA/CN COAGULATION FACTORS (BLOOD)/CN COAGULATION FACTORS V/CN COAGULEN/CN COAGULIN/CN
	=> e coagula E1 E2 E3 E4 E5	1 1	factors xiii/cn 5 COAGULATION FACTOR XIA/CN COAGULATION FACTORS (BLOOD)/CN > COAGULATION FACTORS XIII/CN COAGULEN/CN COAGULIN/CN
	=> e milk fa E1 E2 E3 E4 E5	1	bule egf factor 8/cn 5 MILK BUNDLE-1 PROTEIN (SYNTHETIC)/CN MILK FAT GLOBULE ANTIGEN NP5 (HUMAN FRAGMENT)/CN > MILK FAT GLOBULE EGF FACTOR 8/CN MILK GLASS/CN MILK GROWTH FACTOR/CN
	=> e transcr	iption	nal repressor/cn 5
	E1	1	TRANSCRIPTIONAL REGULATORYPROTEIN (YERSINIA PESTIS STRAIN CO.
	E2	1	TRANSCRIPTIONAL REPRESSION OF HYC AND HYP OPERONS (ESCHERICAL
	E3	0	IA COLI 0157:H7 STRAIN EDL933 GENE HYCA)/CN > TRANSCRIPTIONAL REPRESSOR/CN
	E4	1	TRANSCRIPTIONAL REPRESSOR (AEDES AEGYPTI STRAIN UGAL REDUCED
	E5	1)/CN TRANSCRIPTIONAL REPRESSOR (AGROBACTERIUM TUMEFACIENS STRAIN C58 GENE ACCR)/CN
	=> e E6	1	MDANGOD TOWN COURS
	E0	1	TRANSCRIPTIONAL REPRESSOR (AGROBACTERIUM TUMEFACIENS STRAIN C58 GENE TRAM)/CN
	E7	1	TRANSCRIPTIONAL REPRESSOR (ARABIDOPSIS THALLANA CLONE CLICA
	E8	1	GENE RPD3A)/CN
•		1	TRANSCRIPTIONAL REPRESSOR (ASPERGILLUS ORYZAE STRAIN TK3 GEN E CREA)/CN
]	E9	1	TRANSCRIPTIONAL REPRESSOR (BACILLUS HALODURANS STRAIN C-125
.]	E10	1	GENE BHU826)/CN
		-	TRANSCRIPTIONAL REPRESSOR (BACILLUS HALODURANS STRAIN C-125 GENE BH0847)/CN
	E11	1	TRANSCRIPTIONAL REPRESSOR (BACTERIOPHAGE .PHI.CH1)/CN
1	E12	1	TRANSCRIPTIONAL REPRESSOR (BETA-GALACTOSIDASE GENE) (BACILLU S HALODURANS STRAIN C-125 GENE LACR)/CN
F	E13	1	TRANSCRIPTIONAL REPRESSOR (BRUCELLA MELITENSIS STRAIN 16M GE
Ţ	E14	1	NE BMEIIU46)/CN
1	71.4	1	TRANSCRIPTIONAL REPRESSOR (BRUCELLA MELITENSIS STRAIN 2308 G ENE ERID)/CN
E	15	1	TRANSCRIPTIONAL REPRESSOR (BUTTERFLY GENE EXTRA SEX COMBS) /C
E	216	1	IN .
		_	TRANSCRIPTIONAL REPRESSOR (CANDIDA ALBICANS CLONE P371 GENE TUP1 REDUCED)/CN
E	17	1	TRANSCRIPTIONAL REPRESSOR (CANDIDA UTILIS STRAIN NRRL Y1084 GENE MIG1)/CN
=	> s transcri	nt i on:	al repressor 2/an

=> s transcriptional repressor ?/cn L2 171 TRANSCRIPTIONAL REPRESSOR ?/CN



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=> e "ae-binding protein-1"/cn 5
E1
             1
                    AE-100/CN
E2
              1
                    AE-3/CN
E3
              0 --> AE-BINDING PROTEIN-1/CN
E4
              1
                   AE-CELLULOSE/CN
E.5
              1
                   AE-F 117233/CN
=> e neurophilins 1/cn 5
E1
                    NEUROPEPTIDE, SUBOESOPHAGEAL GANGLION (BOMBYX MORI BOMPBAN G
             1
                    AMMA-)/CN
E2
             1
                    NEUROPEPTIDE-GLUTAMIC ACID-ISOLEUCINE/CN
EЗ
             0 --> NEUROPHILINS 1/CN
F.4
             1
                  NEUROPHYSIN (BUFO JAPONICUS CLONE PVT-1 REDUCED)/CN
E.5
           . 1
                    NEUROPHYSIN (BUFO JAPONICUS CLONE PVT-4 REDUCED)/CN
=> e neurophilins 2/cn 5
E1
             1
                    NEUROPEPTIDE, SUBOESOPHAGEAL GANGLION (BOMBYX MORI BOMPBAN G
                    AMMA-)/CN
F2
             1
                   NEUROPEPTIDE-GLUTAMIC ACID-ISOLEUCINE/CN
E3
             0 --> NEUROPHILINS 2/CN
F.4
             1
                   NEUROPHYSIN (BUFO JAPONICUS CLONE PVT-1 REDUCED)/CN
E5
             1
                   NEUROPHYSIN (BUFO JAPONICUS CLONE PVT-4 REDUCED)/CN
=> e discoidin domain/cn 5
E.1
             1
                   DISCOGUATTINE/CN
E2
                   DISCOIDIC ACID/CN
             1
E3
             0 --> DISCOIDIN DOMAIN/CN
E4
             1
                   DISCOIDIN DOMAIN RECEPTOR 1 KINASE/CN
E5
                   DISCOIDIN DOMAIN RECEPTOR 1 KINASE (HUMAN GENE DDR1 ISOENZYM
             1
                   E DDR1D C-TERMINAL FRAGMENT)/CN
=> e
E6
             1
                   DISCOIDIN DOMAIN RECEPTOR 1 KINASE (HUMAN GENE DDR1 ISOENZYM
                   E DDR1E FRAGMENT)/CN
E7
                   DISCOIDIN DOMAIN RECEPTOR 2 KINASE/CN
             1
E8
             1
                   DISCOIDIN DOMAIN RECEPTOR KINASE (HUMAN GENE CAK ISOENZYME C
                   AK II)/CN
E9
             1
                   DISCOIDIN DOMAIN RECEPTOR KINASE (MUS MUSCULUS STRAIN C57BL
                   GENE CAK ISOENZYME CAK I)/CN
E10
             1
                   DISCOIDIN DOMAIN RECEPTOR KINASE (MUS MUSCULUS STRAIN C57BL
                   GENE CAK ISOENZYME CAK II)/CN
E11
                   DISCOIDIN DOMAIN RECEPTOR TYROSINE KINASE/CN
             1
E12
                   DISCOIDIN DP1 (DICTYOSTELIUM DISCOIDEUM STRAIN AX2)/CN
             1
E13
             1
                   DISCOIDIN I-A (DICTYOSTELIUM DISCOIDEUM REDUCED)/CN
E14
             1
                   DISCOIDIN I-C (DICTYOSTELIUM DISCOIDEUM REDUCED)/CN
E15
                   DISCOIDIN II (DICTYOSTELIUM DISCOIDEUM CLONE D2)/CN
             1
E16
             1
                   DISCOKIOLIDE A/CN
E17
                   DISCOKIOLIDE B/CN
=> s e4-11
             1 "DISCOIDIN DOMAIN RECEPTOR 1 KINASE"/CN
             1 "DISCOIDIN DOMAIN RECEPTOR 1 KINASE (HUMAN GENE DDR1 ISOENZYME
               DDR1D C-TERMINAL FRAGMENT) "/CN
             1 "DISCOIDIN DOMAIN RECEPTOR 1 KINASE (HUMAN GENE DDR1 ISOENZYME
               DDR1E FRAGMENT)"/CN
             1 "DISCOIDIN DOMAIN RECEPTOR 2 KINASE"/CN
             1 "DISCOIDIN DOMAIN RECEPTOR KINASE (HUMAN GENE CAK ISOENZYME CAK
               II)"/CN
             1 "DISCOIDIN DOMAIN RECEPTOR KINASE (MUS MUSCULUS STRAIN C57BL
               GENE CAK ISOENZYME CAK I)"/CN
             1 "DISCOIDIN DOMAIN RECEPTOR KINASE (MUS MUSCULUS STRAIN C57BL
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GENE CAK ISOENZYME CAK II)"/CN

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1 "DISCOIDIN DOMAIN RECEPTOR TYROSINE KINASE"/CN
L3
             8 ("DISCOIDIN DOMAIN RECEPTOR 1 KINASE"/CN OR "DISCOIDIN DOMAIN
               RECEPTOR 1 KINASE (HUMAN GENE DDR1 ISOENZYME DDR1D C-TERMINAL
               FRAGMENT) "/CN OR "DISCOIDIN DOMAIN RECEPTOR 1 KINASE (HUMAN
               GENE DDR1 ISOENZYME DDR1E FRAGMENT) "/CN OR "DISCOIDIN DOMAIN
               RECEPTOR 2 KINASE"/CN OR "DISCOIDIN DOMAIN RECEPTOR KINASE (HUMA
               N GENE CAK ISOENZYME CAK II) "/CN OR "DISCOIDIN DOMAIN RECEPTOR
               KINASE (MUS MUSCULUS STRAIN C57BL GENE CAK ISOENZYME CAK I)"/CN
               OR "DISCOIDIN DOMAIN RECEPTOR KINASE (MUS MUSCULUS STRAIN C57BL
               GENE CAK ISOENZYME CAK II) "/CN OR "DISCOIDIN DOMAIN RECEPTOR
               TYROSINE KINASE"/CN)
=> e nhp/cn 5
E1
             1
                   NHJ 44/CN
                   NHMO/CN
F.2
             1
E3
             0 --> NHP/CN
                   NHP2/RS6-LIKE PROTEIN (TRYPANOSOMA BRUCEI STRAIN 427 GENE NH
E4
             1
                   P2)/CN
F5
             1
                   NHPTT/CN
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=> s (11 or cub domain protein) and (coagulat? factor? or blood coagulation or milk
fat globule egf factor 8 or mfg human milk or transcriptional repressor or crtr-1
protein or ae-binding protein 1 or neurophilin?)
L4
             O FILE MEDLINE
L5
             1 FILE HCAPLUS
L6
             O FILE BIOSIS
L7
             O FILE EMBASE
1.8
             O FILE JICST-EPLUS
EXCEEDS MAXIMUM FIELD LENGTH, WILL BE SEARCHED AS 'CUB-DOMAIN-CONTAINING PROTEIN
RP43 (RIFTIA PACHYPTILA/CN'
EXCEEDS MAXIMUM FIELD LENGTH, WILL BE SEARCHED AS 'CUB-DOMAIN-CONTAINING PROTEIN
RP43 (RIFTIA PACHYPTILA/CN'
L9
             1 FILE WPIDS
TOTAL FOR ALL FILES
L10
             2 (L1 OR CUB DOMAIN PROTEIN) AND (COAGULAT? FACTOR? OR BLOOD COAGU
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Searched by: Mary Hale 308-4258 CM-1 1E01

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LATION OR MILK FAT GLOBULE EGF FACTOR 8 OR MFG HUMAN MILK OR TRANSCRIPTIONAL REPRESSOR OR CRTR-1 PROTEIN OR AE-BINDING PROTEIN 1 OR NEUROPHILIN?)

=> dup rem 110
PROCESSING COMPLETED FOR L10
L11 1 DUP REM L10 (1 DUPLICATE REMOVED)

=> d cbib abs

L11 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2002 ACS DUPLICATE 1 Document No. 134:321614 Protein and cDNA sequences of a novel human CUB-domain containing protein and uses thereof in diagnosis, therapy and drug screening. Donoho, Gregory; Turner, C. Alexander, Jr.; Nehls. Michael; Friedrich, Glenn; Zambrowicz, Brian; Sands, Arthur T. (Lexicon Genetics Incorporated, USA). PCT Int. Appl. WO 2001029219 A1 20010426, 33 CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 2000-US28798 20001008. PRIORITY: US 1999-PV160285 19991019; US 2000-PV183583 20000218. This invention provides protein and cDNA sequences for newly identified human proteins, designated NHPs, which shares structural similarity with animal CUB domain proteins, coagulation factors V and XIII, milk fat globule-EGF factor 8, 5 transcriptional repressor AEbinding protein-1, and neuropilins 1 and 2 (which, like the presently described protein, contain both CUB and

Which, like the presently described protein, contain both CUB and discoidin domains). While NHP shares sequence homol. with other CUB-domain contg. proteins, its primary sequence is unique. Its expression is detected in human cell lines, and human prostate, pituitary, fetal brain, brain, thymus, spleen, lymph node, trachea, kidney, fetal liver, thyroid, adrenal gland, salivary gland, stomach, small intestine, colon, muscle, heart, mammary gland, adipose, skin, esophagus, bladder, cervix, rectum, and testis cells. In one embodiment, the invention relates to diagnostic assays for detecting diseases assocd. with inappropriate NHP activity or levels. Also disclosed are methods for utilizing NHP in drug screening assays and in therapy directed against diseases assocd. with inappropriate NHP activity or levels.

 \Rightarrow s (11 or cub domain protein) and (discoidin domain or 13 or discoidin receptor or ddr2 gene product?)

L12 0 FILE MEDLINE
L13 1 FILE HCAPLUS
L14 0 FILE BIOSIS
L15 0 FILE EMBASE
L16 0 FILE JICST-EPLUS

EXCEEDS MAXIMUM FIELD LENGTH, WILL BE SEARCHED AS 'DISCOIDIN DOMAIN RECEPTOR KINASE (MUS MUSCULUS STRAIN/CN'

EXCEEDS MAXIMUM FIELD LENGTH, WILL BE SEARCHED AS 'DISCOIDIN DOMAIN RECEPTOR KINASE (MUS MUSCULUS STRAIN/CN'

EXCEEDS MAXIMUM FIELD LENGTH, WILL BE SEARCHED AS 'DISCOIDIN DOMAIN RECEPTOR KINASE (MUS MUSCULUS STRAIN/CN'

Searched by: Mary Hale 308-4258 CM-1 1E01

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EXCEEDS MAXIMUM FIELD LENGTH, WILL BE SEARCHED AS 'DISCOIDIN DOMAIN RECEPTOR KINASE (MUS MUSCULUS STRAIN/CN'

EXCEEDS MAXIMUM FIELD LENGTH, WILL BE SEARCHED AS 'DISCOIDIN DOMAIN RECEPTOR KINASE (MUS MUSCULUS STRAIN/CN'

EXCEEDS MAXIMUM FIELD LENGTH, WILL BE SEARCHED AS 'DISCOIDIN DOMAIN RECEPTOR KINASE (MUS MUSCULUS STRAIN/CN'

EXCEEDS MAXIMUM FIELD LENGTH, WILL BE SEARCHED AS 'DISCOIDIN DOMAIN RECEPTOR KINASE (MUS MUSCULUS STRAIN/CN'

L17 O FILE WPIDS

TOTAL FOR ALL FILES

L18 1 (L1 OR CUB DOMAIN PROTEIN) AND (DISCOIDIN DOMAIN OR L3 OR DISCOI DIN RECEPTOR OR DDR2 GENE PRODUCT?)

=> s 118 not 110 L19 O FILE MEDLINE

L20 O FILE HCAPLUS L21 0 FILE BIOSIS

L22 0 FILE EMBASE

0 FILE JICST-EPLUS L23 O FILE WPIDS L24

TOTAL FOR ALL FILES

L25 0 L18 NOT L10

=> (11 or cub domain or extracellular domain or ecd) and (novel human protein? or

(L1 IS NOT A RECOGNIZED COMMAND

The previous command name entered was not recognized by the system. For a list of commands available to you in the current file, enter "HELP COMMANDS" at an arrow prompt (=>).

=> s (l1 or cub domain or extracellular domain or ecd) and (novel human protein? or nhps)

L26 1 FILE MEDLINE L27 7 FILE HCAPLUS L28 1 FILE BIOSIS L29 1 FILE EMBASE L30 O FILE JICST-EPLUS

EXCEEDS MAXIMUM FIELD LENGTH, WILL BE SEARCHED AS 'CUB-DOMAIN-CONTAINING PROTEIN RP43 (RIFTIA PACHYPTILA/CN'

EXCEEDS MAXIMUM FIELD LENGTH, WILL BE SEARCHED AS 'CUB-DOMAIN-CONTAINING PROTEIN RP43 (RIFTIA PACHYPTILA/CN' L31 1 FILE WPIDS

TOTAL FOR ALL FILES

11 (L1 OR CUB DOMAIN OR EXTRACELLULAR DOMAIN OR ECD) AND (NOVEL HUMAN PROTEIN? OR NHPS)

=> s 132 not (110 or 118) L33 1 FILE MEDLINE L34 6 FILE HCAPLUS L35 1 FILE BIOSIS L36 1 FILE EMBASE L37 0 FILE JICST-EPLUS L38 O FILE WPIDS

Searched by: Mary Hale 308-4258 CM-1 1E01

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	• (

TOTAL FOR ALL FILES 9 L32 NOT (L10 OR L18) => dup rem 139 PROCESSING COMPLETED FOR L39 6 DUP REM L39 (3 DUPLICATES REMOVED) => d cbib abs 1-6 L40 ANSWER 1 OF 6 HCAPLUS COPYRIGHT 2002 ACS Document No. 136:162371 Cloning and characterization of novel human protein kinase family members 32374 and 18431 and their therapeutic uses. Meyers, Rachel; Kapeller-Libermann, Rosana; Silos-Santiago, Immaculada (Millennium Pharmaceuticals, Inc., USA). PCT Int. Appl. WO 2002010401 A2 20020207, LR, LS, LT, LO, LV, MA, MID, MG, MIA, MIN, MM, MA, MIA, NO, NA, PL, FI, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2.

APPLICATION: WO 2001-US23653 20010727. PRIORITY: US 2000-PV221543 20000728. The invention provides isolated nucleic acids mols., designated 32374 or AB 18431 nucleic acid mols., which encode novel protein kinase family members. The invention also provides antisense nucleic acid mols., recombinant expression vectors contg. 32374 or 18431 nucleic acid mols., host cells into which the expression vectors have been introduced, and nonhuman transgenic animals in which a 32374 or 18431 gene has been introduced or disrupted. Their putative function domains are analyzed and their gene expression profiles are provided. The invention still further provides isolated 32374 or 18431 proteins, fusion proteins, antigenic peptides and anti-32374 or -18431 antibodies. Diagnostic methods utilizing compns. of the invention are also provided. L40 ANSWER 2 OF 6 HCAPLUS COPYRIGHT 2002 ACS Document No. 136:80918 Protein and cDNA sequences of a novel 2002:10647 human CUB domain-containing protein sequence homolog and uses thereof. Kapeller-Libermann, Rosana (Millennium Pharmaceuticals, Inc., USA). PCT Int. Appl. WO 2002000843 A2 20020103, 107 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2001-US20055 20010621. PRIORITY: US 2000-PV213963 20000623. The invention provides protein and cDNA sequences of a novel human protein, designated 56739, which has sequence

human protein, designated 56739, which has sequence homol. with CUB family members. The invention also provides antisense nucleic acid mols., recombinant expression vectors contg. 56739 nucleic acid mols., host cells into which the expression vectors have been introduced, and nonhuman transgenic animals in which a 56739 gene has been introduced or disrupted. The invention still further provides isolated 56739 proteins, fusion proteins, antigenic peptides and anti-56739 antibodies. Diagnostic methods utilizing compns. of the invention are also provided.

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L40 ANSWER 3 OF 6 HCAPLUS COPYRIGHT 2002 ACS
2001:526099
            Document No. 135:117953 cDNA and protein sequence of
     novel human protein TANGO416 and TANGO457 and
     their uses in drug screening, therapeutics and diagnosis. Fraser,
    Christopher C.; Kirst, Susan J. (Millennium Pharmaceuticals, Inc., USA).
     PCT Int. Appl. WO 2001051514 A1 20010719, 217 pp. DESIGNATED STATES: W:
    AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU,
    CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN,
    IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK,
    MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM,
    TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ,
    TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA,
    GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR.
    (English). CODEN: PIXXD2. APPLICATION: WO 2001-US485 20010105.
    PRIORITY: US 2000-479249 20000107; US 2000-559497 20000427.
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The invention provides cDNA and protein sequence of two novel human protein TANGO416 and TANGO457. The protein TANGO416 was cloned from human fetal spleen and has high homol. with murine protocadherin. Both proteins are transmembrane proteins and contq. extracellular, transmembrane and intracellular domain. These nucleic and proteins are useful for diagnosis, prevention, and therapy of a no. of human and other animal disorders. The invention also provides antisense nucleic acid mols., expression vectors contg. the nucleic acid mols. of the invention, host cells into which the expression vectors have been introduced, and non-human transgenic animals in which a nucleic acid mol. of the invention has been introduced or disrupted. The invention still further provides isolated polypeptides, fusion polypeptides, antigenic peptides and antibodies. Diagnostic, screening, and therapeutic methods using compns. of the invention are also provided. The nucleic acids and polypeptides of the present invention are useful as modulating agents in regulating a variety of cellular processes.

L40 ANSWER 4 OF 6 HCAPLUS COPYRIGHT 2002 ACS 2001:300759 Document No. 134:321609 Protein and cDNA sequences of human secretory proteins and uses thereof in diagnosis, therapy and drug screening. Turner, C. Alexander, Jr.; Donoho, Gregory; Nehls, Michael; Hilbun, Erin; Zambrowicz, Brian; Sands, Arthur T. (Lexicon Genetics Incorporated, USA). PCT Int. Appl. WO 2001029084 A2 20010426, 63 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 2000-US28803 20001018. PRIORITY: US 1999-PV160106 19991018; US 1999-PV162547 19991029. This invention provides protein and cDNA sequences for newly identified AΒ human proteins, designated NHPs, which shares structure motifs typical of human secreted proteins that share structural similarity with animal chordins, NEL protein, and thrombospondin. Also disclosed is another novel human protein that shares structural similarity with animal protein that contains CUB domain. In one embodiment, the invention relates to diagnostic assays for detecting diseases assocd. with inappropriate NHP activity or levels. Also disclosed are methods for utilizing NHP in drug screening assays and in therapy directed against diseases assocd. with inappropriate NHP activity or levels.

L40 ANSWER 5 OF 6 HCAPLUS COPYRIGHT 2002 ACS 1998:608707 Document No. 129:215729 Cloning of cDNA for novel

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human proteins belong to tumor necrosis factor receptor superfamily. Tada, Hideaki; Konishi, Mikio; Fukushima, Daikichi (Ono Pharmaceutical Co., Ltd., Japan). PCT Int. Appl. WO 9838304 A1 19980903, 54 pp. DESIGNATED STATES: W: JP, KR, US; RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE. (Japanese). CODEN: PIXXD2. APPLICATION: WO 1998-JP799 19980226. PRIORITY: JP 1997-43143 19970227. The cDNA for proteins OAF065.alpha. and OAF065.beta. are isolated from ΑB human stroma cell line HAS303. OAF065.alpha. consists of 416 and OAF065.beta. of 423 amino acids, with identical N-terminal 1-415 residues. The C-terminal Glu-Ala of OAF065.alpha. is substituted with 8 amino acid residues in OAF065.beta.. Both protein contains a Cys-rich domain, commonly seen in the extracellular domain of the TNF receptor superfamily. Claimed are methods of recombinant prepn. of the proteins, (monoclonal) antibody to the proteins, oligonucleotide hybridizing to the cDNA, and therapeutics contg. the protein and/or the antibodies.

L40 ANSWER 6 OF 6 MEDLINE DUPLICATE 1
96394649 Document Number: 96394649. PubMed ID: 8798755. Cloning and characterization of islet cell antigen-related protein-tyrosine phosphatase (PTP), a novel receptor-like PTP and autoantigen in insulin-dependent diabetes. Cui L; Yu W P; DeAizpurua H J; Schmidli R S; Pallen C J. (Cell Regulation Laboratory, Institute of Molecular and Cell Biology, National University of Singapore, 10 Kent Ridge Crescent, Singapore 0511, Republic of Singapore.) JOURNAL OF BIOLOGICAL CHEMISTRY, (1996 Oct 4) 271 (40) 24817-23. Journal code: 2985121R. ISSN: 0021-9258. Pub. country: United States. Language: English.

Cloning of the cDNA encoding a novel human protein- tyrosine phosphatase (PTP) called islet cell antigen-related PTP (IAR) predicts a receptor-like molecule with an extracellular domain of 614 amino acids containing a hydrophobic signal peptide, one potential N-glycosylation site, and an RGDS peptide which is a possible adhesive recognition sequence. The 376-amino acid intracellular region contains a single catalytic domain. Recombinant IAR polypeptide has phosphatase activity. Northern blot analysis shows tissue-specific expression of two IAR transcripts of 5.5 and 3. 7 kilobases, which are most abundant in brain and pancreas. The IAR PTP is homologous in its intracellular region to IA-2, a putative PTP that is an insulin-dependent diabetes mellitus (IDDM) autoantigen. IAR is also reactive with IDDM patient sera. IAR and IA-2 may distinguish different populations of IDDM autoantibodies since they identify overlapping but nonidentical sets of IDDM patients. Thus IAR is likely to be an islet cell antigen useful in the preclinical screening of individuals for risk of IDDM.

=> s (11 or cub domain or extracellular domain or ecd) and (agonist or antagonist)
L41 611 FILE MEDLINE
L42 485 FILE HCAPLUS
L43 408 FILE BIOSIS
L44 359 FILE EMBASE

EXCEEDS MAXIMUM FIELD LENGTH, WILL BE SEARCHED AS 'CUB-DOMAIN-CONTAINING PROTEIN RP43 (RIFTIA PACHYPTILA/CN'

EXCEEDS MAXIMUM FIELD LENGTH, WILL BE SEARCHED AS 'CUB-DOMAIN-CONTAINING PROTEIN RP43 (RIFTIA PACHYPTILA/CN' L46 203 FILE WPIDS

TOTAL FOR ALL FILES

L47 2102 (L1 OR CUB DOMAIN OR EXTRACELLULAR DOMAIN OR ECD) AND (AGONIST

Searched by: Mary Hale 308-4258 CM-1 1E01

36 FILE JICST-EPLUS

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OR ANTAGONIST)
=> s 147 and (13 or discoidin(w) (receptor! or domain))
L48
              O FILE MEDLINE
L49
               1 FILE HCAPLUS
L50
               O FILE BIOSIS
L51
               O FILE EMBASE
L52
               O FILE JICST-EPLUS
EXCEEDS MAXIMUM FIELD LENGTH, WILL BE SEARCHED AS 'DISCOIDIN DOMAIN RECEPTOR KINASE
(MUS MUSCULUS STRAIN/CN'
EXCEEDS MAXIMUM FIELD LENGTH, WILL BE SEARCHED AS 'DISCOIDIN DOMAIN RECEPTOR KINASE
(MUS MUSCULUS STRAIN/CN'
EXCEEDS MAXIMUM FIELD LENGTH, WILL BE SEARCHED AS 'DISCOIDIN DOMAIN RECEPTOR KINASE
(MUS MUSCULUS STRAIN/CN'
EXCEEDS MAXIMUM FIELD LENGTH, WILL BE SEARCHED AS 'DISCOIDIN DOMAIN RECEPTOR KINASE
(MUS MUSCULUS STRAIN/CN'
EXCEEDS MAXIMUM FIELD LENGTH, WILL BE SEARCHED AS 'DISCOIDIN DOMAIN RECEPTOR KINASE
(MUS MUSCULUS STRAIN/CN'
L53
               O FILE WPIDS
TOTAL FOR ALL FILES
               1 L47 AND (L3 OR DISCOIDIN(W) (RECEPTOR! OR DOMAIN))
=> d cbib abs
L54 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2002 ACS
1998:71221 Document No. 128:136859 Soluble ErbB receptor
     extracellular domain fusion proteins their uses in
     antagonization of growth factors. Fizpatrick, Vincent Danial; Sliwkowski,
     Mark; Vandlen, Richard L. (Genentech, Inc., USA). PCT Int. Appl. WO
     9802540 Al 19980122, 58 pp. DESIGNATED STATES: W: AL, AM, AT, AU, AZ,
     BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW:
     AT, BE, BF, BJ, CF, CG, CH, CI, CM, DE, DK, ES, FI, FR, GA, GB, GR, IE,
     IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 1997-US11825 19970708. PRIORITY: US 1996-21640
     19960712: US 1997-798326 19970210.
     Sol. heteromultimeric immunoadhesin fusion proteins that contain the
     extracellular ligand-binding domains of ErbB receptors oligomerized via
     the multimerization domains of Igs are described for use as
     antagonists of neuregulins in the control of cell proliferation,
     e.g. in cancers. Specifically, the extracellular
     domains of ErbB2 and ErbB3 or ErbB2 and ErbB4 are used in
     combination. The prepn. ErbB/IgG fusion proteins and the characterization
     of their heregulin binding properties is reported.
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=> s donoho, g?/au,in;s turner, c?/au;s nehls, m?/au,in;s friedrich, g?/au,in
'IN' IS NOT A VALID FIELD CODE
L55
             6 FILE MEDLINE
L56
         . 44 FILE HCAPLUS
L57
            9 FILE BIOSIS
'IN' IS NOT A VALID FIELD CODE
L58
            5 FILE EMBASE
L59
             O FILE JICST-EPLUS
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Searched by: Mary Hale 308-4258 CM-1 1E01

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36 FILE WPIDS
L60
TOTAL FOR ALL FILES
          100 DONOHO, G?/AU, IN
L62
          1091 FILE MEDLINE
L63
          1428 FILE HCAPLUS
L64
          1198 FILE BIOSIS
L65
           772 FILE EMBASE
L66
             7 FILE JICST-EPLUS
L67
           212 FILE WPIDS
TOTAL FOR ALL FILES
L68
          4708 TURNER, C?/AU
'IN' IS NOT A VALID FIELD CODE
L69
            38 FILE MEDLINE
L70
            77 FILE HCAPLUS
L71
            42 FILE BIOSIS
'IN' IS NOT A VALID FIELD CODE
            30 FILE EMBASE
L72
L73
            O FILE JICST-EPLUS
L74
            39 FILE WPIDS
TOTAL FOR ALL FILES
L75
          226 NEHLS, M?/AU, IN
'IN' IS NOT A VALID FIELD CODE
L76
           158 FILE MEDLINE
           337 FILE HCAPLUS
L77
L78
           163 FILE BIOSIS
'IN' IS NOT A VALID FIELD CODE
1.79
           167 FILE EMBASE
1.80
            1 FILE JICST-EPLUS
1.81
           105 FILE WPIDS
TOTAL FOR ALL FILES
           931 FRIEDRICH, G?/AU, IN
=> s 161 and 168 and 175 and 182
L83
             O FILE MEDLINE
L84
            10 FILE HCAPLUS
L85
             0 FILE BIOSIS
L86
             O FILE EMBASE
L87
            0 FILE JICST-EPLUS
L88
            10 FILE WPIDS
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TOTAL FOR ALL FILES

L89 20 L61 AND L68 AND L75 AND L82

=> dup rem 189
PROCESSING COMPLETED FOR L89
L90 10 DUP REM L89 (10 DUPLICATES REMOVED)

=> d 1-10 cbib abs

L90 ANSWER 1 OF 10 HCAPLUS COPYRIGHT 2002 ACS DUPLICATE 1 2001:360153 Document No. 134:363350 Characterization and applications of novel human proteases. Donoho, Gregory; Hilbun, Erin; Turner,

Searched by: Mary Hale 308-4258 CM-1 1E01

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- C. Alexander, Jr.; Nehls, Michael; Friedrich, Glenn; Zambrowicz, Brian; Sands, Arthur T. (Lexicon Genetics Incorporated, USA). PCT Int. Appl. WO 2001034779 A2 20010517, 34 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2000-US31179 20001109. PRIORITY: US 1999-PV165260
- AB The cDNA sequences and corresponding deduced amino acid sequences of novel human proteases (NHPs) are disclosed. The NHP genes were obtained from a human testis cDNA library using probes and/or primers generated from human gene trapped sequence tags. The described NHPs share significant similarity to a variety of mammalian proteases, and esp. carboxypeptidase A. The NHPs can be used in therapeutic, diagnostic, and pharmacogenomic applications.
- L90 ANSWER 2 OF 10 HCAPLUS COPYRIGHT 2002 ACS DUPLICATE 2
 2001:360152 Document No. 134:363349 Characterization of novel human ATPase homologs. Donoho, Gregory; Turner, C. Alexander, Jr.; Hilbun, Erin; Nehls, Michael; Friedrich, Glenn; Zambrowicz, Brian; Sands, Arthur T. (Lexicon Genetics Incorporated, USA). PCT Int. Appl. WO 2001034778 A2 20010517, 45 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, WO 2000-US31110 20001109. PRIORITY: US 1999-PV164624 19991110.
- The present invention relates to the discovery, identification, and characterization of novel human proteins which share structural similarity with calcium transporting ATPases and aminophospholipid transporters. The cDNA sequences and the corresponding deduced amino acid sequences of the human ATPase homologs are disclosed. The human ATPase homologs can be used in therapeutic, diagnostic, and pharmacogenomic applications.
- L90 ANSWER 3 OF 10 HCAPLUS COPYRIGHT 2002 ACS

 2001:338573 Document No. 134:348997 Protein and cDNA sequences of human transport proteins and uses thereof in diagnosis, therapy and drug screening. Harras, Marie; Donoho, Gregory; Turner, C.

 Alexander, Jr.; Nehls, Michael; Friedrich, Glenn;
 Zambrowicz, Brian; Sands, Arthur T. (Lexicon Genetics Incorporated, USA).
 PCT Int. Appl. WO 2001032706 A2 20010510, 59 pp. DESIGNATED STATES: W:
 AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English).
 CODEN: PIXXD2. APPLICATION: WO 2000-US29852 20001031. PRIORITY: US
- AB This invention provides protein and cDNA sequences for newly identified human proteins, designated NHPs, which share structural similarity with mammalian multi-drug resistance (MDR) proteins and cellular transporters. In one embodiment, the invention relates to diagnostic assays for detecting diseases assocd. with inappropriate NHP activity or levels.

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Also disclosed are methods for utilizing NHP in drug screening assays and in therapy directed against diseases assocd. with inappropriate NHP activity or levels. Seq ID No. 47 and 48 were claimed, but information was not provided.

L90 ANSWER 4 OF 10 HCAPLUS COPYRIGHT 2002 ACS DUPLICATE 4
2001:300872 Document No. 134:321614 Protein and cDNA sequences of a novel human CUB-domain containing protein and uses thereof in diagnosis, therapy and drug screening. Donoho, Gregory; Turner, C. Alexander, Jr.; Nehls, Michael; Friedrich, Glenn; Zambrowicz, Brian; Sands, Arthur T. (Lexicon Genetics Incorporated, USA). PCT Int. Appl. WO 2001029219 Al 20010426, 33 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 2000-PV183583 20000218.

AB This invention provides protein and cDNA sequences for newly identified human proteins, designated NHPs, which shares structural similarity with animal CUB domain proteins, coagulation factors V and XIII, milk fat globule-EGF factor 8, 5 transcriptional repressor AE-binding protein-1, and neuropilins 1 and 2 (which, like the presently described protein, contain both CUB and discoidin domains). While NHP shares sequence homol. with other CUB-domain contg. proteins, its primary sequence is unique. Its expression is detected in human cell lines, and human prostate, pituitary, fetal brain, brain, thymus, spleen, lymph node, trachea, kidney, fetal liver, thyroid, adrenal gland, salivary gland, stomach, small intestine, colon, muscle, heart, mammary gland, adipose, skin, esophagus, bladder, cervix, rectum, and testis cells. In one embodiment, the invention relates to diagnostic assays for detecting diseases assocd. with inappropriate NHP activity or levels. Also disclosed are methods for utilizing NHP in drug screening assays and in therapy directed against diseases assocd. with inappropriate NHP activity or levels.

L90 ANSWER 5 OF 10 HCAPLUS COPYRIGHT 2002 ACS

2001:247518 Document No. 134:276537 Protein and cDNA sequences of human carboxypeptidases and uses thereof in diagnosis, therapy and drug screening. Donoho, Gregory; Turner, C. Alexander, Jr.; Nehls, Michael; Friedrich, Glenn; Zambrowicz, Brian; Sands, Arthur T. (Lexicon Genetics Incorporated, USA). PCT Int. Appl. WO 2001023588 Al 20010405, 36 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXDZ. APPLICATION: WO 2000-US26876 20000929. PRIORITY: US 1999-PV156685 19990929.

AB This invention provides protein and cDNA sequences for newly identified human proteins, designated NHPs, which shares substantial sequence homol. with animal proteases, esp. carboxypeptidases. While NHP shares sequence homol. with other carboxypeptidases, its primary sequence is unique. Its expression is detected in various human tissues including brain, pituitary, spinal cord, thymus, spleen, lymph node, bone marrow, trachea, lung, kidney, prostate, testis, thyroid, adrenal gland, stomach, small intestine colon, skeletal muscle, uterus, mammary gland, bladder, cervix cells, and gene trapped human cells. In one embodiment, the invention

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relates to diagnostic assays for detecting diseases assocd. with inappropriate NHP activity or levels. Also disclosed are methods for utilizing NHP in drug screening assays and in therapy directed against diseases assocd. With inappropriate NHP activity or levels.

- L90 ANSWER 6 OF 10 HCAPLUS COPYRIGHT 2002 ACS

 DUPLICATE 6

 2001:247510 Document No. 134:261891 Protein and cDNA sequences of human serine/threonine protein kinase and uses thereof in diagnosis, therapy and drug screening. Donoho, Gregory; Turner, C. Alexander, Jr.;

 Nehls, Michael; Friedrich, Glenn; Zambrowicz, Brian; Sands, Arthur T.

 (Lexicon Genetics Incorporated, USA). PCT Int. Appl. Wo 2001023579 A1

 20010405, 38 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 2000-US26621 20000927. PRIORITY: US 1999-PV156511 19990928.
- AB This invention provides protein and cDNA sequences for newly identified human proteins, designated NHPs, which shares substantial sequence homol. with animal kinases, and more particular serine/threonine protein kinases. While NHP shares sequence homol. with other serine/threonine protein kinases, its primary sequence is unique. Its expression is detected in various human tissues including brain, pituitary, spinal cord, spleen, trachea, kidney, prostate, testis, adrenal gland cells, and gene trapped human cells. In one embodiment, the invention relates to diagnostic assays for detecting diseases assocd. with inappropriate NHP activity or levels. Also disclosed are methods for utilizing NHP in drug screening assays and in therapy directed against diseases assocd. with inappropriate NHP activity or levels.
- L90 ANSWER 7 OF 10 HCAPLUS COPYRIGHT 2002 ACS

 DUPLICATE 7

 2001:247499 Document No. 134:261870 Protein and cDNA sequences of a novel human organic anion transport protein. Turner, C. Alexander, Jr.; Donoho, Gregory; Wattler, Frank; Nehls, Michael;

 Friedrich, Glenn; Zambrowicz, Brian; Sands, Arthur T. (Lexicon Genetics Incorporated, USA). PCT Int. Appl. WO 2001023566 A1 20010405, 31 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 2000-US26630 20000927. PRIORITY: US 1999-PV156161 19990927.
- AB This invention provides protein and cDNA sequences for newly identified human proteins, designated NHPs, which shares substantial sequence homol. with animal org. anion, and more particularly prostaglandin, transporter proteins. While NHP shares sequence homol. with other org. anion transport proteins, its primary sequence is unique. Its expression is detected in various human tissues including brain, pituitary, spinal cord, lymph node, trachea, heart, adipose, skin, pericardium, hypothalamus cells, and gene trapped human cells. In one embodiment, the invention relates to diagnostic assays for detecting diseases assocd. with inappropriate NHP activity or levels. Also disclosed are methods for utilizing NHP in drug screening assays and in therapy directed against diseases assocd. with inappropriate NHP activity or levels.

L90 ANSWER 8 OF 10 HCAPLUS COPYRIGHT 2002 ACS DUPLICATE 8



- 2001:229020 Document No. 134:262848 Cloning and characterization of human endothelin converting enzyme-like proteins. Donoho, Gregory;
 Turner, C. Alexander, Jr.; Nehls, Michael; Friedrich, Glenn; Zambrowicz, Brian; Sands, Arthur T. (Lexicon Genetics Incorporated, USA). PCT Int. Appl. WO 2001021773 A2 20010329, 31 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 2000-PV176689 20000118.
- AB Novel human endothelin converting enzyme-like proteins of 255 and 883 amino acids in length and cDNAs encoding these proteins are disclosed. The endothelin converting enzyme-like proteins and encoding nucleic acids can be used in therapeutic, diagnostic, and pharmacogenomic applications.
- L90 ANSWER 9 OF 10 HCAPLUS COPYRIGHT 2002 ACS DUPLICATE 9
 2001:228919 Document No. 134:247996 Protein and cDNA sequences for a novel human protease inhibitor-like protein NHP and use thereof. Donoho,
 Gregory; Turner, C. Alexander, Jr.; Wattler, Frank; Nehls, Michael;
 Friedrich, Glenn; Zambrowicz, Brian; Sands, Arthur T. (Lexicon Genetics Incorporated, USA). PCT Int. Appl. WO 2001021651 A2 20010329, 29 pp.
 DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 2000-US26048
 20000922. PRIORITY: US 1999-PV156101 19990924.
- AB The invention provides protein and cDNA sequences for a novel human protease inhibitor-like protein NHP that can be used in therapeutic, diagnostic, and pharmacogenomic applications.
- L90 ANSWER 10 OF 10 HCAPLUS COPYRIGHT 2002 ACS DUPLICATE 10
 2001:168158 Document No. 134:189017 Protein and cDNA sequences of human calcium dependent protease homologs, and uses thereof in therapy, diagnosis and drug screening. Donoho, Gregory; Turner, C.
 Alexander, Jr.; Nehls, Michael; Friedrich, Glenn; Zambrowicz, Brian; Sands, Arthur T. (Lexicon Genetics Incorporated, USA). PCT Int. Appl. WO 2001016336 A1 20010308, 39 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 2000-US24062 20000901. PRIORITY: US 1999-PV152057 19990902.
- AB The invention provides protein and cDNA sequences of a novel class of human calcium dependent protease homologs which share structural similarity with animal calcium dependent proteases, or calpains. The novel calcium dependent protease homolog encoding cDNAs were obtained from human gene trap clones and human cDNA libraries. The invention further relates to the uses of calcium dependent protease homolog in therapy, diagnosis and drug screening.



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